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RESULT 1 AX148306 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE FEATURES JOURNAL CDS source Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. AX148306 1800 bp Sequence 5 from Patent EP1116794. AX148306 AX148306.1 GI:14347193 l (bases 1 to 1800) Inchi,S., Kobayashi,M. and Shinozaki,K. Transgenic plants carrying neoxanthin cleavage enzyme gene patent: Ep 1116794-A 5 18-JUL-2001; Riken (JP) thale cress. /organism="Arabidopsis thaliana" /db_xref="taxon:3702" /note="unnamed protein product" Location/Qualifiers .1800 .1800 DNA linear PAT 08-JUN-2001

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Direct Submission
Submitted (22-APR-1999) Satoshi Tuchi, RIKEN, Plant
3-1-1 Kouyadai. Tsukuba 305-0074, Japan
(E-mail:iuchi@rtc.riken.go.jp, Tel:81-298-36-4359)
Location/Qualifiers
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Iuchi,S., Kobayashi,M. and Shinozaki,K.
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FEATURES	REFERENCE AUTHORS TITLE JOURNAL COMMENT	VERSION VERSION KEYWORDS SOURCE ORGANISM ORGANISM REFERENCE AUTHORS TITLE JOURNAL	Qy 1681 Db 3511 (Qy 1741) Db 3571 (Db 3571) RESULT 3 AB028617/c LCCUS	Qy 1441 Db 3271 Qy 1501 Db 3331 Qy 1561 Db 3391 Qy 1621 Db 3451
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c-MOA2 Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'. The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/Grail-1.3/), GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and SplicePredictor (Volker Brendel, Stanford University, http://gremlin1.zool.iastate.edu/cgi-bin/sp.cgi). Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE/). This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is MLN21 and the 3' clone is MIE1.	2 (bases 1 to 52232) 2 (bases 1 to 52232) Sato,S., Nakamura,Y., Kaneko,T., Kato,T., Asamizu,E. and Tabata,S. Direct Submission Submitted (09-JUN-1999) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934) Address for correspondence: kaos@kazusa.or.jp For the latest information on annotation of this clone, please see	AB028617.1 GI:5041970 Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui Pl clone:MOA2. Marabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (sites) Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty pl and TAC clones DNA Res. 7 (2), 131-135 (2000)	cagatagttaacgccgttagcgttgaagcaacggttaaacttccgtcaagggtt 1740	gtcaacagaaacatgctcggccgtaaaaccaaattcgcttacttggctttagccgagccg 1500
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NHTATASPHLSKHIQNALYRARYHNLEILVAREYISFYEQEEDHDETLLKFAKLNFNY

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FIMTWNTHQYSRSIRGCCEIKKKKKVVLCSLLIHRYSNYSLVHVLRCFVFLYNSIFLC
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Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Yamamura,Y.,
Yu,G., Yu,S., Bowser,L., Carninci,P., Chen,H., Cheuk,R.,
Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,
Kawai,J., Kim,C., Koesema,E., Lam,B., Lin,J., Meyers,M.C.,
Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,
Satou,M., Seki,M., Shinn,P., Southwick,A., Tracy,S.E.,
Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
Direct Submission
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                                                                                                                     Submitted (12-SEP-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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Salk, Stanford, PGEC (SSP) Consortium members carried
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Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIS. sequencing and annotation of the RAFL cDNAs: Yamada,K., Banh,J., Banno,F., Dale,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Yamamura,Y., Yu.G., Yu.S., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Koesema,E., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Tracy,S.E., Davis,R.W., Ecker,J.R. and Theologis,A. ç

/organism="Arabidopsis
/db_xref="taxon:3702" thaliana'

5'UTR source ecotype: Columbia" (FLC-1) as a BamHI/XhoI insert. /clone="RAFL08-11-H16 (R11094)" /note="This clone is in a modif /gene="MOA2.4/AT3g14440" /chromosome="3" modified pBluescript

gene

/gene="MOA2.4/AT3g14440" 123. .1922

/evidence=experimental /gene="MOA2.4/AT3g14440" /codon_start=1

KVDLTTGEVKKHLYGDNRYGGEPLFLPGEGGEEDEGYILCFVHDEKTWKSELQIVNAV SLEVEATVKLPSRVPYGFHGTFIGADDLAKQVV" /product="putative 9-cis-epoxycarotenoid dioxygenase"
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/db_xref="GI:15810433" EIRLNLKTGESTRRPIISNEDQQVNLEAGMVNRNMLGRKTKFAYLALAEPWPKVSGFA

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/note="560 c 533 g 62:
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1800	cgtacggatttcacggtacattcatcggagccgatgatttggcgaagcaggtcgtgtg	7	Qy
1862	CAGATAGTTAACGCCGTTAGCGTTAGAGGTTGAAGCAACGGTTAAACTTCCGTCAAGGGTT	1803	Db
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1742	CTTTACGGCGATAACCGTTACGGAGGAGAGCCTCTGTTTCTCCCCCGGAGAAGGAGAG	1683	Дb
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1622	GTCAACAGAAACATGCTCGGCCGTAAAACCAAATTCGCTTACTTGGCTTTAGCCGAGCCG	UT.	DЬ
1500	Caacagaaacatgctcggccgtaaaaccaaattcgcttacttggctttagccgagcc	1441	Qy
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REFERENCE
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Johnson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bei, B., Chin, C.,
Chiou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N.,
Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, J.,
Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H.,
Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M.,
Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J.

Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J.

Direct Submission

AL Submitted (24-MAY-2000) Arabidopsis thaliana Genome Center,
Department of Biology, University of Pennsylvania, 38th and
Hamilton Walk, Philadelphia, PA 19104-6018, USA

Chouk, R., Shinn, P., Brooks, S., Buehler, E., Chao, Q.,
Chouson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bei, B., Chin, C.,
Chiou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N.,
Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, J.,
Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Sakano, H.,
Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                             Submitted (26-MAY-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (07-FEB-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Str Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
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Genomic sequence for Arabidopsis thaliana BAC F3F9 from chrom
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Ecker, J.R.
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                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                   2000 this sequence version replaced
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BAC F3F9 from chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
/product="F3F9.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EELSIECF"
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/db_xref="GI:8052549"
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FELEAKVEQVIPPVKVEDGESTTHETRRMRYGEEFLSSRLCRPPMVTGLEKSLDLSSS
                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAF71812.1"
/db_xref="GI:8052548"
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/db_xref="GI:8052530"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(8524. 8759,8846. 9287)
/note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /evidence=not_experimental
/product="F3F9.3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=not_experimental
/product="F3F9.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to dioxygenase
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                                                                             .21156))
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protein; similar and gb|AA586078.]
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                                      gb|T41672.1,
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Query Match
Best Local Similarity
Matches 1139; Conserv
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                                                           TCCAAATAGCCGGGAACTTCTTCCCGGTACCGGAGAAACCTGTCGTGCATAACCTTCCGG
                                                                                                 ttcagatcgccggaaattttgctccggtgaatgaacagcccgtccggcgtaatcttccgg
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tggtcggaaaacttcccgattccatcaaaggagtgtatgtgcgcaacggagctaacccac
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FVRFSRLTRIKSINSKWGLLRFSVQHFDITRVNIKAPGDSPWTDGIKIGSSNHMKIH
HVDLATGDDCIAILSGTFNLDINKNGCFGHGISVGSLKFKGEKSVQGLIVRNSIFN
GTSNGVRIKTWPSPGEBNLVSNFLFKNLQMIDVQSPINIDQRYCPNPCSFQVTSLTR
GTSNGVRIKTWPSPGEBNLVSNFLFKNLQMIDVGSFNVQLFNINIVHRGRDGPATS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MTITIISGMYIYSLLSQDAHHSQYGQNTNLVLKKPIPKPQTAA FNQESTMASTILLPSTSTQFLDRTFSTSSSSSRPKLQSLSFSSTLRNKKLVVPCYVSS SVNKKSSVSSLQSPFKPGSWKKLCNDVFNLIPKTRNQNPKLNPVQRTAAWTUDAVE NAMISHERRHHPHFKTADPAVQIAGNEFPVPEKPVVHNLPVTGTVPECLGVEVRNGA NPLHKPVSGHHLFDGGMVHAVRFDNGSVSVACRFTETNRLVQEREGGRPVFVKAIGE LHGHLGIAKLMLFNTRGLFGLVDPTGGLGVANAGLVYFNGHLLAMSEDDLPYHVKVTQ TGDLETSGRYDFDGQLKSTMIAHPKIDPETRELFALSYDVVSKPYLKYFRFTSDGEKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to 9-cis-epoxycarotenoid gb|AAF26356.1"
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join(26752. .26907,27020. .27871,27923. .28153)

note-"similar to exopolygalacturonase precursor
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/db_xref="G1:8052547"
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/db_xref="GI:8052533"
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/product="F3F9.10"
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73.1%;
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Pred. No. 2.1e-245;
0; Mismatches 407;
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                                                                                                                                                                                                                                                                                                                                           aagtcgttttcaagctgccggagatgatccgcggtgggtctccggtggtttacgacaaga
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                                                                                                                                                                                                              CAGACGAGGTTGTCGTGATTGGATCATGCATGACGCCACCTGATTCAATTTTCAACGAAC
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Iuchi,S., Kobayashi,M. and Shinozaki,K.
Transgenic plants carrying neoxanthin cleavage Patent: EP 1116794-A 15 18-JUL-2001;
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//Protein_id="CAC41199.1"
//db_xref="G1:14347204"
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//translation="MATTTSHATNIWIKTKLSMDSSKSSTSKWNLYQKAAAMAL
NINSSLQAPPILHFPKQSSNYQOFRNGSASYACRFTETERLYQEKIFKCVQGYVVR
NGANDLFEPTACHHFPGDGMWHAVQFKNGSASYACRFTETERLYQEKALGRVYFPKA
IGELHGHSGIARLMLFYARGLFGLYDHSKGTGVANAGLVYFNNRLLAMSEDDLPYHVK
VTPTGDLKTEGRFDFDGQLKSTMIAHPKLDPVSGELFALSTDVIOKPYLKYFRFSKMG
EKSHDVEIPVEDFTMHDFAITENFVIPDQQVYFKMSEMIRGGSPVYDOKNKYSRFG
ILDKYAKDGSDLKWVEVPDCFCFHLWNAWEEAETDEIVVIGSCMTPPDSIFNECDEGL
KSVLSEIRLNLKTGKSTRKSIIENDEGVNLEAGMVNRKHLGRKTEYANIAIAEPWPK
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                                                                                           Direct Submission

Submitted (09-JAN-1998) Burbidge A., The University of Submitted (09-JAN-1998) Burbidge A., The University of Physiology and Environmental Science, Sutton Bonington Loughborough, Leicestershire, LE12 SRD, UK
On Jan 13, 1998 this sequence version replaced gi:2243:
                                                                                                                                                                                                                                                                                                                                                                                                                        Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                               Burbidge,A., Grieve,T.M., Jackson,A., Thompson,A. and Taylor,I.B. Structure and expression of a cDNA encoding a putative neoxanthin cleavage enzyme (NCE) isolated from a wilt-related tomato (Lycopersicon esculentum Mill.) library J. Exp. Bot. 47, 2111-2112 (1997)
                                                                                                                                                                                                    Direct Submission
Submitted (01-JUL-1997) Burbidge A., The University of Physiology and Environmental Science, Sutton Bonington Loughborough, Leicestershire, LE12 5RD, UK
Revised by [3]
(pases 1 to 2171)
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Z97215.1 GI:2769641
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435 c 431 g 617 t
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742

682 589 622

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SOURCE
ORGANISM
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potato.
Solanum tuberosum
Eukaryota; Viridi
                                            AJ276244.1 GI:7209268
9-cis-epoxycarotenoid
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Solanum tuberosum mRNA
dioxygenase (ncedl gene
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   Viridiplantae;
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Streptophyta;
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9-cis-epoxycarotenoid
Embryophyta;
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Tracheophyta;
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Best Local Similarity 70.7%;
Matches 1093; Conservative
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809.4; No. 8.8

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Spermatophyta; Magnoliophyta; eudicotyledons; or Asteridae; euasterids I; Solanales; Solanaceae; losaes I to 2164)
Burbidge, A., Taylor, I.B. and Thompson, A.
Potato putative 9-cis-epoxycarotenoid dioxygenas
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'/product" plative 9-cis-epoxycarotenoid dioxygenase"
//protein_id="CAB76920.1"
//db_xref="G1:7209269"
//db_xref="G1:7209269"
//translation="MATTTSHATNTWIKPKLSMPSSKEFGFASNSISLLKNQHNROSL
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GANPLEEPTAGARFFDODGMVHAVOFKNGSASYACFTFETERFVQEKALGFPVEPKAI
GELHGHSGIARLMLFYARGLFGLIDHSRGTGVANAGLVYFNNRLLAMSEDDLPYHVKV
TPTGDLKTEGRFDDGQLKSTMLAHPKLDPVSGELFALSYDVIQKYLKYFFSKNGE
KSNDVELFVEDDTWAHDFAITEKFYLIFDQQVVFKMSEMIRGGSPVVLDKNVSBREGI
LDKYAKDGSDLKWVEVPDCFCFHLWNAWEEPETDEIVVIGSCMTPPDSIFNECDEGLK
SVLSEIRLNLKTGKSTBRAIIENPDEQVNLEAGMVNRNKLGRKTQYAYLLAIAEPWRKV
SGFAKVDLFTGEVEKEIYGDNKYGGEPLFLEPDPNSKEEDDGYILAFVHDEKEWTSEL
QIVNAWTIKLBATVKLPSRVPYGFHGTFINANDLANQA"
67 a 437 c 433 g 627 t
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/function="cleavage
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73. 1887
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                                 TTAATGCAATGACTTTAAAGTTAGAGGCAACAGTGAAACTTCCATCAAGAGTTCCTTATG
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          ACGCCGTGAAGTTCACGAACGGCGCCGCCAGCTACGCCTGCCGCTTCACCGAGACGCAGC
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Transgenic plants carrying neoxanthin cleavage
Patent: EP 1116794-A 11 18-JUL-2001;
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Submitted (16-JUL-1999) Satoshi Iuchi, RIKEN, Plan
3-1-1 Kouyadai, Tsukuba 305-0074, Japan
(E-mail:iuchi@rtc.riken.go.jp, Tel:81-298-36-4359)
Location/Qualiflers
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CSLQTLHFPKQYQPTSTSTSTATTTTPPPIKTTTTTTPPPRETMPLSDTNQPLPQKW
NFLQKAAATALDLVETALVSHERKHPLPKTKADPRVQ IAGNFAPVPEHAADGLPVVGK
IPKCLDGVYVRNGANFLYEPVACHHFFDGDGMYHAVKFTNGAASYACRFTETQRLSQE
KSLGRPVFPKAIGELHGHSGIARLLEYARGLEGLVDGSOGMYANAGLVYFNNHLLA
MSEDDLPYHVRITPNGDLTTVGRYDFNQQLUSTMIAHPKLDPVDGDLHALSYDVIGKP
YLKYERFSPDGVKSPQVEIPLKEPTMMHDFATTENFVVVPDQQVYFKLTEMITGGSPV
YYDKNKTSRFGILHKNAKDANAMRWIDAPDCFCFHLWNAWEEPETEEVVVIGSCMTPA
DSIIFNECEESLKSYLSEIRLNLRTGKSTRRPIISDAEQVULEAGKVNRNKIGRKTOFA
LALALBEWRKVSGFAKVDLLSGEVKKYMYGEEKFGGEPLFLPNGQKEDDGYILAFVHD
EKEWKSELQIVNAQNIKLEASIKLPSRVPYGFHGTFIHSKDLRKQA"

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/protein_id="BAB11932.1"
/db_xref="GI:9857290"
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The 9-cis-epoxycarotenoid cleavage reaction is the key restep of abscisic acid biosynthesis in water-stressed bean Proc. Natl. Acad. Sci. U.S.A. 96 (26), 15354-15361 (1999) 20079657
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Direct Submission
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State University, Wilson Str., E
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/function="catalyzes the oxidative cleavage
double bond of 9-cis-epoxycarotenoids (C40)
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                                    VGKIPKCIDGYYVRNGANPLYEPVAGHHFFDGDGMVHAVKFTNGAASYACRFTETQRLAQEKSLGRPVFPKAIGELHGHSGIARLLLFYARSLFQLVDGSHGMGVANAGLVYFNNHLLAMSEDDLPYHVRITSNGDLTTVGRYDFNGQLNSTMIAHPKLDPVNGDLHALSYDVV
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         AGAAGCCTTACCTCAAGTACTTCCGTTTCTCCGCTGACGGCGTAAAGTCCCCCGACGTCG
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Town,C.D. and Kaul,S.
Direct Submission
Submitted (15-JUL-2000)
Medical Center Dr, Rockv
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Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and
Arabidopsis thaliana chromosome 1 BAC T2H7 genomic seque
                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Arabidopsis thaliana
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Eukaryota; Viridiplantae;
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SA, cdtown@tigr.
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genomic
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Utterback,T.
                                                                                            sequence
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Submitted (19-JAN-2001) The Institute for Genomic Research, Submitted (conter Dr. Rockville, MD 20850, USA, cdtcwn@tigr.org
On Jan 19, 2001 this sequence version replaced gi:12280878.
Address all correspondence to:at@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genes were identified by a combination of several methods: Gene prediction programs including Genscan+ (Chris Burge, http://CCR-081.mit.edu/GENSCAN.html), GenemarkHMM (Mark Borodovsky, http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant of GlimmerM, see Mihaela Pertea,
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Town, C.D. and Kaul, S.
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                                                   complement(3313...366)
/rpt_family="AT_rich"
complement(436...4686)
/rpt_family="AT_rich"
complement(5249...5270)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(729...1868)
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(Arabidopsis thaliana)"
                                                                                                                                                                                                                                                                                                  AIRPSESKKEVCDASWLSDAFEEPFGTVAKMLIKRRTYCLEMNSF complement(2328...2392)
                                                                                                                                                                                                                                                                                                                                                                                  KDLGRCCIVSRREHSLVPFVENVLVRVDCVISDDDSSSSDENHRFSLNTASISDAGGA
GGSFSALFRLVFAPIFKPFQMLGQILGPKRSSSSFDASFSAINDEIGVTHHSPTQVLK
NFGEIRFLKIELPTGEBLGILKKWRADPGSTLDNCMILGASSVLQSNVKNHENS
VDEDNGNIPESFYTNGGLKLRVVWTISSLIAASARHYLLQPIINEHKSLDRLVLSDAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(729. .1868)
/gene="T2H7.1"
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                               complement(<7213. .>8049)
                                                                                                                                                                                                                                                  /rpt_family="AT_rich"
2828. .2894
                                                                                                                                                                                                                                                                                                                                                              GQGVLCMNREQLEELRVTPLSASSASKRTLVPALNMRLWYAPELDLPDGTVLKGATLV
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/db_xref="61:1321627"
/translation="MSYLLRSDPVSRIHPEPQSLTSFDHFDLLPDSLLLLLIFDKVADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(<729. .>1868)
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/cultivar="Columbia"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:3702"
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complement(13002. 16330)
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/note="predicted |
complement(7213.
/gene="T2H7.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family "ATCOPIA121 ATCOPIA12I Internal region ATCOPIA12 LTR-retrotransposon." complement(14311. 14498) /rpt_family="ATCOPIA13I ATCOPIA13I Internal region ATCOPIA13 LTR-retrotransposon." complement(15657. .16345)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="AT_rich"
complement(11013. .11070)
/rpt_family="-"-"
                                                                                                   /rpt_family="(CAAAAA)n"
complement(join(<19380.
/gene="T2H7.4"
                                                                                                                                                                                                                                                                                                  IGEIVLYDPAKQELLNLTDKPIPEEIVTAKWIGASKGWAFFLDTQDRCVLITDSLNPW
ACKSNPKLLTLPPLNPLFSCQTDVIWNVAMSSCPDDDEDWVVGIKSLGDQVSFCRPRR
DLRWTKFQTPSDHFPTSNLTYSKRDRKFYLPGPGGHHLLSYDLDFNKADQPEFHELQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="ATCOPIA14||ATCOPIA14| Internal region ATCOPIA14 LTR-retrotransposon." join(<17486. .17518,17796. .18535,18620. .>18947) /gene="T2H7.3" 17486. .18947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(14226. 14687)
/rpt_family="ATCOPIA221|ATCOPIA221 -
sequence."
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/rpt_family="ATCOPIA14I|ATCOPIA14I Internal region of
ATCOPIA14 LTR-retrotransposon."
complement(14032. .14866)
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/rpt_family="AT_rich"
complement(10873. .10
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/rpt_family="AT_rich"
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PIPVLTYRENTKDGEIKNPKDVEFRNPEEEDEPMVKDIICVSPPEKIVRVVSEKKQRD
DVAMEEYKPVTEQTLASEEACNTRNHVNPNKPYGRSKSDKPRRKRLSVDTETTKRKSY
                                                                                                                                                                                            complement(17528. .17576)
                                                                                                                                                                                                                   FMVFREEETTEERFMCYTDDIGDLCIFVSKSEAFCVPASSYPGLKPNSIYFVGFGLGI
YDLTTRNVSIFRAPKGALNQIVSPYWFPPASS"
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/note="similar to hypothetical protein GI:8778720 from
(Arabidopsis thaliana)"
                                                                               complement(19380. .20533)
                                                                                                                                                                                                                                                                         RNFPESLKYDSELSELFPSSCRTERFVESPSGDERFLVKWYAKGCLASSSKITYETQR
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                                                                                                                                                                                                                                                                                                                                                                                        translation="MSRLLSKLSPLIHKRSVRSFSSSTTGPYLQLSLSAKPSSEGVVN/
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.8049)
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              gccggtatagtcgacccggcacacggaaccgggtgtagctaacgccggtttggtctatttc
                                                                           ggtgagcttcacggccacaccggtattgcccgactcatgctattctacgccagagctgca
                                                                                                                                                                                                                                                cgcaacggagctaacccacttcacgagccggtgacaggtcaccacttcttcgacggagac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aagcccaaagccaaagaatccaacactaaacagatgaatttgttccagagagcggcggcg
                                                                                                                       GAAACCGAGAGATTGGTTCAAGAGAAACAACTCGGTTCTCCGATTTTCCCTAAAGCTATA
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                                                                                                                                                                                                                                                                                                                                                                                           AACCCCATAATTCCCGAAAAAGACACTTCCCGTTGGAACCCTCTCCAACGCGCCGCCTCC
TTCGGTTTATTAAATCACAAAAACGGAACCGGAGTTGCTAACGCCGGTTTGGTTTACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCGCACTCGACTTCGCCGAAACCGCATTGTTAAGACGCGAACGTTCTAAACCTCTCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(21856. .24837)
/gene="T2H7.5"
/gene="TiH7.5"
/note="similar to En Spm like transposon protein
GI:4115361 from (Arabidopsis thaliana)"
complement()oin(21856. .2230,22534. .22806,2304;
23290. .23520,24442. .24837))
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IVMVFREEETKDGRKNMRYIDDIGDLCIFISKGEDFCVKASSCPGLQPNSISLHGRLF
AILMLIKRTMGCYEYPQGIPKRIPYLPYMLPPFSP"
complement(21599. .21620)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(19380. .19710,19799.
/gene="TZH7.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(<21856. .22030,22534. 23290. .23520,24442. .>24837))
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/rpt_family="AT_rich"
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PYASKSKPKMIHLPFFTPMYSGQTEVVCNVAMSSPPPDQDDDHEDWVVGIKFLGRQLS
LCRPRHDLRWTNILTPFESWEVSELMYSKKDQRFYLLAPGGNYLCSWDLNFKEDKKPK
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               GAAAAACGATTGGGTCGACCAGTTTTCCCGAAAGCAATCGGCGAGCTTCACGGTCACTCG
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1752)
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Patent: EP
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Transgenic plants carrying neoxanthin c
Patent: EP 1116794-A 1 18-JUL-2001;
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//db_xref="01:143/7190"
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RVQLAGNYSPVPESSYRRNLTYVEGTIPDCIDCYYIRNQANPMFEPTAGHHLFDGDGMV
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GLINNQNGVGYANAGLYYFNNELLAMSEDDLPYQLKITQTGDLQTYGRYDDFDGQLKSA
MIAHPKLDPVTKELHALSYDVVKKPYLKYFRESPDGVKSPELEIPLETPTMHDFAIT
ENFVVIPDQQVVFKLGEMISGKSPVFDGEKVSRIGIMPKDATEASQIIWNSPETFC
FLWNAMESPETEEITVIGSCMSPADSIFNENDDSLRSVLSEIRLNLTTRKTTRSSLL
VNEDYNLEIGMYNRNELGRKTBRFFLAIAYPRKVSGFAKVDLCTGEMKKYIYGGEKY
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/db_xref="taxon:3702"
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REFERENCE
AUTHORS
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Direct Submission
Submitted (03-FEB-1998) MIPS, at the Max-Planck-Institut fuer Submitted (03-FEB-1998) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, Proj Coordinator: Mike Bevan, Molecular Genetics Department, Cambri Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, te-mail: michael.bevan@bbsrc.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLINNQNGVGVANAGLVYFNNRLLAMSEDDLPYQLKITQTGDLQTVGRYDFDGQLKSA
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                                                                                         note="strong similarity to (S)-2-hydroxy-acid oxidase
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                                                            .3.15), peroxisomal,
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Best Local Similarity 68.2
Matches 1063; Conservative
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ggaggaggaggaagacgaaggatacatcctctgtttcgttcacgacgaggaagacatggaaa
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Unpublished
2 (bases 1
                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: Lemcke@mips.biochem.mpg.de.mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 38835;
Murphy,G., Ridley,P.,
Mayer,K.F.X.
                                                                                                                                                                                                                                Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/this fragment has an overlap with ATCHRIV47 at the 5' end an overlap with ATCHRIV49 at the 3' end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 107966 to 194143)

Hilbert,H., Braun,M., Holzer,E., Brandt,A., Duesterhoeft,A., Mewes,H.W., Lemcke,K. and Mayer,K.F.X.
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AL161548
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8542

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chromophore

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EEIKTLPLNGDRVKLQLILADLLRNIVNHAPFPNSWVGISISPGQELSRDNGRYIHLQ
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Matches 1063;
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1144 aaggtcgcaagattcgggattttagacaaatacgccgaagattcatcgaacattaagtgg 1203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cagatcgccggaaattttgctccggtgaatgaacagcccgtccggcgtaatcttccggtg 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATCCTCTCCGGCTAAACATCTTCCAGAAAGCGGCGGCGATTGCGATCGACGCGGCTGAG 110204
                                                                                                                                                                                                                                                                                                                                              GGACGTTACGATTTCGACGGTCAGTTAAAATCCGCAATGATAGCTCACCCGAAACTGGAC 110804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cacggaaccggtgtagctaacgccggtttggtctatttcaatggccggttattggctatg 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAAAACGATTGGGTCGACCAGTTTTCCCGAAAGCAATCGGCGAGCTTCACGGTCACTCG 110564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gaacgtcaattgggtcgaccggttttccccaaagccatcggtgagcttcacggccacacc 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ttcgaacacggttcagctagctacgcttgccggtttactcagactaaccggtttgttcag
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                                                           gtcgttttcaagctgccggagatgatccgcggtgggtctccggtggtttacgacaagaac 1143
                                                                                                                                  ccaacgatgatgcacgatttcgcgattacagagaaacttcgtcgtcgtacctgaccagcaa 1083
                                                                                                                                                                                                               tacttccgattctcaccggacggaactaaatcaccggacgtcgagattcagcttgatcag 1023
                                                                                                                                                                                                                                                                     CCGGTTACGAAGGAGCTTCACGCGTTAAGCTACGACGTCGTTAAGAAAACCTTACCTGAAA 110864
                                                                                                                                                                                                                                                                                    ccggaatccggtgaactcttcgctttaagctacgacgtcgtttcaaagccttacctaaaa 963
                                                                                                                                                                                                                                                                                                                                                                   ggtcggttcgattttgatggacaattagaatccacaatgattgcccacccgaaagtcgac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATAACCAACGGTTCAGCTAGCTACGCATGCCGGTTTACAAAAACCGAGAGATTGGTTCAG 110504
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                                       GTCGTGTTCAAGCTCGGCGAGATGATTTCCGGTAAATCTCCGGTTGTTTTCGACGGAGAA 111044
                                                                                                                CCGACGATGATTCACGATTTCGCTATAACGGAGAATTTTGTGGTGATTCCTGATCAACAA 110984
                                                                                                                                                                                           TACTTCAGATTCTCGCCAGACGGCGTTAAATCGCCGGAATTGGAGATCCCGCTCGAAACT 110924
                                                                                                                                                                                                                                                                                                                                                                                                                       TCAGAAGACGATTTACCGTACCAATTAAAAATTACTCAAACCGGCGATCTCCAAACCGTT 110744
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/gene="AT4g18140"
/number=3
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/gene="AT4g18140"
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68.2%;
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Pred. No. 3.6e-208;
0; Mismatches 478;
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DЪ QΥ Db Š 망 δÃ Ъ δÃ δÃ В Ş В Ş В 8 망 δÃ Ф δõ В 밁 111285 111045 AAGGTTTCCCGATTGGGGATAATGCCCAAGGACGCGACAGAAGCTTCTCAGATAATCTGG 111104 111579 111519 111459 111399 111339 111165 111105 111639 1612 1564 tacggcgataaccgttacggaggagagcctctgtttctccccgg-----agaa 1611 1504 1444 1384 1204 attgatgctccagattgcttctgcttccatctctgggaacgcttgggaagagccagaaaca 1263 GAAGAAAATGAAGATGACGGTTATATATTTTGTCACGTTCATGACGAAGAAACAAAGACA 111578 ggaggagaggaggacgaaggatacatcctctgtttcgttcacgacgagaagacatggaaa 1671 TACGGCGGTGAGAAATATGGCCGGCGAACCGTTTTTCTTGCCCCGGCAACTCCGGTAACGGC 111518 CCAAAAGTTTCCGGTTTCGCTAAGGTCGATCTTTGCACCGGTGAGATGAAAAAAATATATT 111458 cctaaagtctcaggattcgctaaagttgatctcactactggagaagttaagaaacatctt 1563 ACGCGTCGTTCGTTGGTTAACGAGGAT-----GTAAATTTAGAGATTGGTATGGTT 111338 actcgccgtccgatcatctccaacgaagatcaaccaagtcaacctcgaagcagggatggtc 1443 GTGAACTCTCCGGAGACGTTCTGTTTTCATCTCTGGAATGCATGGGAATCGCCGGAGACG 111164 111638

Search completed: July 24, 2002, 07:42:25 Job time: 7835 sec

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Database
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                   Result
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                  a
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Bd
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798.4
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528.2
229.8
                                                                                                                                                                                                                                                                                                                                    Score
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s derived by a
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1: /SIDS1/gcgdata/gc2: /SIDS1/gcgdata/gc3: /SIDS1/gcgdata/gc3: /SIDS1/gcgdata/gc5: /SIDS1/gcgdata/gc6: /SIDS1/gc6: /SIDS1/gcgdata/gc6: /SIDS1/gc6: 
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length: 2000000000
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                                                                                                                                                                                                                                                                                                                                       Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is the number of results predicted by chance to have a iter than or equal to the score of the result being printed, ived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                   Query
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13744.479 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | SIDSI/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
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| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
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Copyright (c) 1993 - 2000 Compugen Ltd
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
                                                                                                                                                                                                                                                                                                                                       Length DB
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                                                                                          Arabidopsis thalia
Lycopersicon escul
Vigna unguiculata
Arabidopsis thalia
Zea mays neoxanthi
Arabidopsis thalia
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                           Eucalyptus grandis
Rice abscisic acid
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	5653	21	-			45
ucalyptus grandi	5655	21	8		45	44
×	4354	21	0		6	43
otus gr	5647	21	5		8	42
	5651	21	N		9.	41
cadiat	5715	21	311		53.8	40
	5654	21	æ		Ġ	39
	5651	21	0		6	38
	5648	21	4		6.	37
	5652	21	-		σ.	36
Pinus radiata tran	5697	21	0		œ	35
radiata tra	712	21	w		2	34
ta	5694	21	4		6	33
s radiata	5691	21	5			32
Eucalyptus grandis	5654	21	6	٠	5	31
Pinus radiata tran	5690	21	8		7.	30
Pinus radiata tran	5711	21	9			29
	5714	21	0		6	28
Pinus radiata tran	5712	21	0		8	27
radiata	5716	21	9		æ	26
radiata	5716	21	1		106.6	25
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ALIGNMENTS

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                          13-JAN-2000; 2000JP-0010056
11-JAN-2001; 2001JP-0003476
                                                                                                                                                                                    plant growth
                                                                                                                                                                                            Neoxanthin cleavage enzyme; AtNCED3; abscisic acid; ABA; herbicide; stress tolerance; transgenic plant; plant breeding; antisense-therapy;
                                                                                                                                                                                                                         Arabidopsis thaliana neoxanthin cleavage enzyme, AtNCED3 cDNA.
                                                                                                                                                                                                                                             10-SEP-2001
                                                                                                                                                                                                                                                                AAD09396;
                                                                                                                                                                                                                                                                                   AAD09396 standard; cDNA; 1800
        (RIKE ) RIKEN KK
                                                       11-JAN-2001; 2001EP-0300218
                                                                          18-JUL-2001.
                                                                                              EP1116794-A2
                                                                                                                                                                 Arabidopsis thaliana.
                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                    protectant;
                                                                                                                                   Location/Qualifiers
1..1800
                                                                                                                /*tag= a
/product= "Arabidopsis thaliana AtNCED3 protein"
                                                                                                                            /*tag=
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AAC56695

Eucalyptus

grandis

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The invention relates to neoxanthin cleavage enzymes and their corresponding cDNA molecules. Neoxanthin cleavage enzyme plays a key corresponding cDNA molecules. Neoxanthin cleavage enzyme plays a key corle in endogenous abscisic acid (ABA) biosynthesis under drought stress. CC Neoxanthin cleavage enzyme is used for improving stress tolerance in a plant by plant when expressed in a plant cell. The invention also relates to methods for increasing or decreasing stress tolerance in a plant by cc introducing the DNA into the plant, and a transgenic plant into which a cneoxanthin cleavage enzyme is introduced. The improvement of stress cotolerance in plants is useful, for example in plant breeding. Neoxanthin cleavage enzyme genes are useful for producing transgenic plants. An arid land can be improved by growing transformant weed for several years and then removing the weed by specifically lowering stress tolerance in the weed by inducing an inducible promoter. The present cDNA sequence encodes Arabidopsis thaliana neoxanthin cleavage enzyme, AtNCED3 protein.

The AtNCED3 cDNA is obtained from an Arabidopsis plant-derived cDNA library using a cDNA of the CPRD65 (CowPea Responsive to Dehydration) energy can be isolated from cowpea plant as a probe.
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Best Local Similarity 100
Matches 1800; Conservative
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RESULT
AAD09401
           The invention relates to neoxanthin cleavage enzymes and their corresponding cDNA molecules. Neoxanthin cleavage enzyme plays a key role in endogenous abscisic acid (ABA) biosynthesis under drought stress. Neoxanthin cleavage enzyme is used for improving stress tolerance in a plant when expressed in a plant cell. The invention also relates to methods for increasing or decreasing stress tolerance in a plant by introducing the DNA into the plant, and a transgenic plant into which a neoxanthin cleavage enzyme is introduced. The improvement of stress tolerance in plants is useful, for example in plant breeding. Neoxanthin cleavage enzyme genes are useful for producing transgenic plants. An arid land can be improved by growing transformant weed for several years and then removing the weed by growing transformant weed for several years and then removing an inducible promoter. The present cDNA sequence encodes by copersicon esculentum neoxanthin cleavage enzyme, LeNCED1 protein
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corresponding cDNA molecules. Neoxanthin cleavage enzyme plays a key role in endogenous abscisic acid (ABA) biosynthesis under drought stress. Neoxanthin cleavage enzyme is used for improving stress tolerance in a plant when expressed in a plant cell. The invention also relates to methods for increasing or decreasing stress tolerance in a plant by introducing the DNA into the plant, and a transgenic plant into which a neoxanthin cleavage enzyme is introduced. The improvement of stress tolerance in plants is useful, for example in plant breeding. Neoxanthin cleavage enzyme genes are useful for producing transgenic plants. An arid land can be improved by growing transformant weed for several years and then removing the weed by specifically lowering stress tolerance in the weed by inducing an inducible promoter. The present cDNA sequence encodes Vigna unguiculata neoxanthin cleavage enzyme, CPRD65 (CowPea Responsive to Dehydration) protein. CPRD65 gene is isolated from cowpea plant.
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                                                                                                                                                                                                                     The invention relates to neoxanthin cleavage enzymes and their corresponding cDNA molecules. Neoxanthin cleavage enzyme plays a key crole in endogenous abscisic acid (ABA) biosynthesis under drought stress. CN Neoxanthin cleavage enzyme is used for improving stress tolerance in a comethods for increasing or decreasing interest to relates to introducing the DNA into the plant, and a transgenic plant into which a cheavage enzyme is introduced. The improvement of stress tolerance in plants is useful, for example in plant breeding. Neoxanthin cleavage enzyme is useful for producing transgenic plants. An arid cleavage enzyme genes are useful for producing transgenic plants. An arid cleavage enzyme genes are useful for producing transgenic plants. An arid cleavage enzyme weed by growing transformant weed for several years and then removing the weed by specifically lowering stress tolerance in the weed by inducing an inducible promoter. The present cDNA sequence encodes arabidopsis thaliana neoxanthin cleavage enzyme, AtNCED1 protein.

The AtNCED1 cDNA is obtained from an Arabidopsis plant-derived cDNA clibrary using a cDNA of the CPRD65 (CowPea Responsive to Dehydration) are several plant as a probe.
                                                                                                                                   Query Match
Best Local Similarity
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11-JAN-2001;
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neoxanthin cleavage enzyme is introduced. The improvement of stress tolerance in plants is useful, for example in plant breeding. Neoxanthin cleavage enzyme genes are useful for producing transgenic plants. An arid land can be improved by growing transformant weed for several years and then removing the weed by specifically lowering stress tolerance in the weed by inducing an inducible promoter. The present cDNA sequence encodes seem anys neoxanthin cleavage enzyme, VP14 protein related to the
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RESULT AAD0930 XX AAD0 XX AAD0 XX AAD0 XX IO-S XX STAR XX STAR XX STAR XX STAR XX Plan 6

AAD09398 standard; CDNA; 1734 ВP

10-SEP-2001 (first entry)

Arabidopsis thaliana neoxanthin cleavage enzyme, AtNCED5

Neoxanthin cleavage enzyme; AtNCED5; stress tolerance; transgenic plant; p ; abscisic acid; plant breeding; ABA; herbicide; antisense-therapy;

growth protectant; ss.

Location/Qualifiers
1..1734

/product= /*tag= "Arabidopsis thaliana AtNCED5 protein"

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CC corresponding cDNA molecules. Neoxanthin cleavage enzymes and their CC corresponding cDNA molecules. Neoxanthin cleavage enzyme plays a key CC role in endogenous abscisic acid (ABA) biosynthesis under drought stress. CC Neoxanthin cleavage enzyme is used for improving stress tolerance in a cc plant when expressed in a plant cell. The invention also relates to CC methods for increasing or decreasing stress tolerance in a plant by CC introducing the DNA into the plant, and a transgenic plant into which a cc neoxanthin cleavage enzyme is introduced. The improvement of stress tolerance in plants is useful, for example in plant breeding. Neoxanthin CC cleavage enzyme genes are useful for producing transgenic plants. An arid CC land can be improved by growing transformant weed for several years and then removing the weed by specifically lowering stress tolerance in the weed by inducing an inducible promoter. The present cDNA sequence encodes C Arabidopsis thaliana neoxanthin cleavage enzyme, AKUCED5 protein.

The AtNCED5 cDNA is obtained from an Arabidopsis plant-derived cDNA C gene isolated from cowpea plant as a probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to novel plant transcription factors from Eucalyptus grandis or Pinus radiata. The present sequence is the coding sequence for one such transcription factor. The transcription factor may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
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18-AUG-1999;
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and EREBs, zinc finger domains of type 2 Cys2His2, CCAAT
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99US-0149485.
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                      This invention describes a novel polynucleotide sequence (I) which encodes a protein capable of regulating the synthesis of abscisic acid. The invention also describes (1) an oligonucleotide encoding a protein of a gene obtained by controlling the expression of a VP14-like gene; (2) a vector containing the oligonucleotide ligated operably to the regulation sequence; (3) a plant transformed with the vector; and (4) a method for regulating abscisic acid synthesis in a plant including the transfer of the above oligonucleotide to it. The gene is useful for constructing drought resistant rice.
                                                                                                                                                                                                                                                                                                                (NORQ )
                                                                                                                                                                                               Oligonucleotide encoding gene for regulplants, useful for constructing e.g. godrought resistance and ear-germination
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Best Local Similarity
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                                 Wood M,
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18-AUG-1999;
                                                                                                                               09-MAR-2000;
                                                                                                                                                      14-SEP-2000
                                                                                                                                                                            WO200053724-A2
                                                                                                                                                                                                  Eucalyptus grandis
                                                                                                                                                                                                                                                                                              Eucalyptus grandis transcription factor DNA sequence #566
                                                                                                                                                                                                                                                                                                                                                                    AAC56695
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           2000-579369/54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aattagaatccacaatgattgcccacccgaaagtcgacccggaatccggtgaactcttcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGTGCGCGTCACCGCCGACGGCGACCTTCGAGACCGTCGGCCGCTACGACTTCGACGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTACGCGCGCGCCGC - CTCGGCCTCCTCGACCCGTCACACGGCACCGGCGTCGCCAAACG
                                                       GENESIS R
FLETCHER
                                                                                                                                                                                                                                                                                                                                                                    standard;
                                McGrath A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                               2000WO-US06112
                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                           99US-0266513
99US-0149485
                                                       RES & DEV CORP LTD.
R CHALLENGE FORESTS
                                                                                                                                                                                                                                                                                                                                                                    DNA;
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69.7%;
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Pred. No. 2.
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                                                        LTD.
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New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
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Claim 1; Page 494; 747pp; English

Eucalyptus grandis or Pinus radiata. The present sequence is the coding sequence for one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacla, poplar, sweetgum, taak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic helix-loop-helix zipper, homeodic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2 and EREBs, zinc finger domains of type 2 Cys2His2, CCAAT box elements The present invention relates to novel plant transcription factors from

Sequence 372 B₽; 60 A; 148 Ç 101 ຸດ 63 Τ; 0 other;

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Query Match
Best Local Similarity
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361
                        999
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             ggacgtcgagat 1010
                                                            aatgattgcccacccgaaagtcgacccggaatccggtgaactcttcgctttaagctacga
                                                                                                                                                                   tcccaatggagatttaaaaaaccgttggtcggttcgattttgatggacaattagaatccac
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                                                cgtcgtccggaagccgtacctcaagtacttccgattctccaaggacggcgagaagtcccc
                                                                                                   gatgatcgcccacccgaagatcgacccggcttccggcgagatgttcgccctcagctacga
                                                                                                                                                    gcgctccggcgacctcgagaccgtcggccgctacgacttcgccggccagctcgactctcc
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                                                                                                                                                                                                                                                         cctcttcggcctcgtcgaccaccggaatggcatggcgtcgcgaacgccggcctcgtgta
                                                                                                                                                                                                                                                                                                                                                               257;
                                                                                                                                                                                                                                                                                                                                                               Conservative
372
                                                                                                                                                                                                                                                                                                                                                                          10.4%;
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Pred.
                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                          188;
No. 2.
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                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                   300
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                                                   360
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Qy DЪ QУ

Ъ

Qγ Вþ Qy

밁

Qγ

B Qy Ъ Q

AAC56548 standard; DNA;

ВP

25-JAN-2001 (first entry)

Eucalyptus grandis transcription factor DNA sequence #419

RESULT 10
AAC56548
ID AAC565
XX AAC565
XX AC565
XX Eucaly
DT 25-JAN
XX
DE Eucaly
XX
Plant;
KW Poplar
KW poplar
KW basic
KW basic
KW homeoc
KW type;
XX
OS Eucal: poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor; basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain; type 2 Cys2His2; CCAAT box elemant. MADS;

Eucalyptus grandis

SS

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RESULT :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to novel plant transcription factors from Eucalyptus grandis or Pinus radiata. The present sequence is the coding sequence for one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic helix-loop-helix zipper, LIM domain, AP2 and ERBBs, zinc finger domains of type 2 Cys2His2, CCAAT box elements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAR-1999;
18-AUG-1999;
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                    AAC42989 standard; DNA; 1788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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Local Similarity 71.2%;
nes 227; Conservative
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                                                                                                                                                                                                                                                                                                  tgccggttcaccgagacgcaacgcctgatccaggaacggggcctcggccgccccgtcttc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B₽;
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les 92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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05-MAR 1999
09-MAR 1999
23-MAR 1999
23-MAR 1999
24-MAR 1999
06-APR 1999
06-APR 1999
07-APR 1999
23-APR 1999
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24-MAY 1999
25-MAY 1999
26-MAY 1999
27-MAY 1999
21-MAY 1999
21-MAY
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
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18-JUN-1999;
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18-JUN-1999;
18-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hybridisation assay; genetic mapping; gene expression protein identification; signal transduction pathway;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000EP-0301439
9908-012348
9908-0126785
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9908-0130419
9908-0130449
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Best Local Similarity 50.3
Matches 709; Conservative
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27-AUG-1999
27-AUG-1999
31-AUG-1999
31-AUG-1999
31-AUG-1999
31-SEP-1999
11-SEP-1999
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12-SEP-1999
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11-OCT-1999
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573
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                                    gaaacaaaccggagctccggttatgcctaacgtgtttttccggattcaacggtgtaacggc
          acgtcaattgggtcgaccggttttccccaaagccatcggtgagcttcacggccacacccg-
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990S-0151066
990S-0151060
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990S-0160815
990S-0161356
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Pred. No. 6.5e
0; Mismatches
                                                                                                                                              DB .
6.5e-44;
es 634;
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                                                                                                                                                                             Length
                                                                                                                                                           69;
                                                                                                                                                         Gaps
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                                                       605
                   664
                                     572
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ת המה של מה של תר את המה של מה של של של ש

18-JUN 1999
18-JUN 1999
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                                                                                                                                       Neoxanthin oleavage enzyme is used for improving stress tolerance in a plant when expressed in a plant cell. The invention also relates to methods for increasing or decreasing stress tolerance in a plant by introducing the DNA into the plant, and a transgenic plant into which a neoxanthin cleavage enzyme is introduced. The improvement of stress tolerance in plants is useful, for example in plant breeding. Neoxanthin cleavage enzyme genes are useful for producing transgenic plants. An arid land can be improved by growing transformant weed for several years and then removing the weed by specifically lowering stress tolerance in the weed by inducing an inducible promoter. The present cDNA sequence encodes arabidopsis thaliana neoxanthin cleavage enzyme, AtNCED2 cDNA is obtained from an Arabidopsis plant-derived cD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to defence-related signalling genes isolated from the sunflower (Helianthus annuus). The genes encode a neoxanthin cleavage enzyme (NCE), an amino acid permease (AAP) and a glutamic acid rich protein (GRP). The signalling gene is useful for increasing the resistance of a plant to a pathogen such as fungus, virus, bacterium, nematode or insect (e.g. European corn borer), preferably Sclerotinia spp., Phoma spp., or Phomopsis spp., by stably incorporating a specific specifi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                       Eucalyptus grandis or Pinus radiata. The present sequence is the coding sequence for one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic helix-loop-helix zipper, LIM domain, AP2 and EREBS, zinc finger domains of type 2 Cys2His2, CCAAT box elements
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            and
                                                                                                                                                                                                                                                  New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
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New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
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Claim 1: Page 599; 747pp; English.

The present invention relates to novel plant transcription factors from Eucalyptus grandis or plans radiata. The present sequence is the coding sequence for one such transcription factor. The transcription factor mabe used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic helix-loop-helix zipper, homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2 and ERBBs, zinc finger domains of type 2 Cys2His2, CCAAT box elements may

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BM085073 saj31a08.
BE432853 EST399478
BH4559796 BOHRRA7TF
BH458011 BOHBT02TF
BH974879 sai74bi1.
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ALIGNMENTS

ACCESSION VERSION KEYWORDS RESULT 1 BM412731 LOCUS DEFINITION COMMENT FEATURES REFERENCE SOURCE TITLE JOURNAL AUTHORS ORGANISM source 1 (bases 1 to 720) Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Ts., J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato fruit tissue, breaker stage (2002) Contact: CUGI Clemson University Genomics Institute Clemson University Lycopersicon esculentum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; BM412731 720 bp mRNA linear EST 22-JAN-200 EST587047 tomato breaker fruit Lycopersicon esculentum cDNA clone cLEG60N24 5' end, mRNA sequence. BM412731 BM412731.1 GI:18264350 EST. Email: http://www.genome.clemson.edu/orders/index.html This clone is available through the Clemson University Genomics Unpublished (2002) tomato. Seq primer: T3 100 Jordan Hall, Clemson, SC 29634, USA Lycopersicon /db_xref="taxon:4081" /clone="cLEG60N24" /clone_lib="tomato breaker f /tissue_type="Pericarp" /dev_stage="breaker" /note="Vector: pBluescriptSKmCUadapt; Site_1: Site_2: XhoI; supplier: Boyce Thompson Institu /organism="Lycopersicon/cultivar="TA496" /lab_host="SOLR" Location/Qualifiers .720 esculentum" fruit" Institute; EST 22-JAN-2002

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Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato fruit tissue, breaker stage (200)
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            ggagttacagatagttaacgc 1694
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                                                                                                                                                                                                                                                                9712 Medical Center Drive,
Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                       Whole genome shotgun sequencing Unpublished (2001) Other_GSSs: BOGRQ53TR
                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 781)
Town,C.D., Van Aken,S., Utterback,T. and Fra
                                                                                                                                                                                                                                                                                                                                                                       Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; eudicotyledons; brassica.
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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BH549344
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                                                      Similarity
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is from a doubled |
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                                                                                                            204
                                          Conservative
                                                                                                    /organism="Brassica oleracea"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOGRQ53"
/clone_ib="BOGRP53"
/clone_ib="BOGRP51; Site_1: BstXI; 2-3 kb
genomic DNA inserted into pHOS1 using BstXI
104 a 203 c 192 g 182 t
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                                      Score 416.2; repred. No. 4.3e.0; Mismatches
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. No. 4.3e-113;
ismatches 228;
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KEYWORDS
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VERSION
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AW933524
                                                          REFERENCE
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AW933524.2
EST.
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1 (bases 1 to 643)
Alcala,J., Vrebalov,J., White,R., Matern,A.L.,
Upton,J., Hansen,T., Craven,M.B., Bowman,C.L.,
Fraser,C.M., Martin,G.B., Tanksley,S.D. and G
Generation of ESTs from tomato fruit tissue
                                                                                 Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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CDNA clone cLEF5
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                                                                      Lycopersicon
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                          Holt, I.E., Liang, F., Ahn, S., Ronning, C.M.
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                                                                                                             Tracheophyta;
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tcctgtatgactccaccagactcaattttcaacgagtctgacg 1327
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4081"
/clone="cLEF54E2"
/clone_ib="tomato fruit mature green,
/tissue_type="fruit pericarp"
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/cultivar="TA496"
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Pred. No. 3.8e-103;
0; Mismatches 163;
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CCGGTACCGGAAAATCCAGTCTGTCAATCTCTTCCGGTCACCGGAAAAATACCCAAATGT
                    ccggtgaatgaacagcccgtccggcgtaatcttccggttggtcggaaaacttcccgattcc
                                                                              Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Ts, J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato fruit tissue, breaker stage (2002)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; Colamina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="tomato breaker fruit"
/tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
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/cultivar="TA496"
/db_xref="taxon:4081"
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Clemson University
100 Jordan Hall, Clemson, SC 29634, U
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Llang, F., Hansen, T.S.,
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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/clone="cLEG44B9"
/clone_lib="tomato breaker
/tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
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/cultivar="TA496"
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Craven,M.B., Bowman,C.L., Ronning,C.M.,
L., Martin,G.B., Giovannoni,J.J. and Tanksley
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                                                                                                                                                                                                                                                                                    cagggatggtcaacagaaacatgctcggccgtaaaaccaaattcgcttactt
                                                                                                                                                                                                                                                                                                                             tcaacgagtctgacgagaatctcaagagtgtcctgtctgaaatccgcctgaatctcaaaa 1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                         agccagaaacagatgaagtcgtcgtgatagggtcctgtatgactccaccagactcaattt 1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acattaagtggattgatgctccagattgcttctgcttccatctctggaacgcttgggaag 1252
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                                                         Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
              Alcala, J.,
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EST.
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                                                                                                                                                                    EST413439 tomato clone cLEG40L2, m
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  Liang, F.,
                                                                                                                 tomato.
                                          Lycopersicon
                              (bases 1
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  Hansen, T.S.,
                Vrebalov,J.,
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eaker fruit, '
A sequence.
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Craven, M.B.,
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  Bowman, C.L.,
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             der Hoeven, R.S.,
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  Ronning, C.
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                                                                                   Tracheophyta;
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                Holt, I.E.,
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Local Similarity 74.2%;
hes 420; Conservative
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                                                           CAGGGAAATCAACAAGAAAATCCATAATCGAAAACCCGGATGAACAAGTGAATTTAGAAG
                                                                         ccggtgaatcaactcgccgtccgatcatctccaacgaagatcaacaagtcaacctcgaag 1432
                                                                                                                    TCAATGAATGTGATGAAGGGCTAAAGAGTGTTTTATCCGAAATCCGTCTCAATTTGAAAA
                                                                                                                                    tcaacgagtctgacgagaatctcaagagtgtcctgtctgaaatcccgcctgaatctcaaaa 1372
                                                                                                                                                                                  AAGCAGAAACAGATGAAATCGTTGTAATTGGTTCATGTATGACACCACCAGACTCCATTT
                                                                                                                                                                                                 agccagaaacagatgaagtcgtcgtgatagggtcctgtatgactccaccagactcaattt 1312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATACCTCAAGTACTTCAGATTTTCAAAAAATGGGGGAAAAATCAAATGATGTTGAAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cttacctaaaatacttccgattctcaccggacggaactaaaatcaccggacgtcgagattc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prime
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104 c 124 g 154 t
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/tissue_type="Pericarp"
/dev_stage="breaker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:4081"
/clone="cLEG40L2"
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Pred. No. 4.3e-88;
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  al Similarity
409; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BM085672 553 bp mRNA linear EST 19-NOV-20 saj28a02.y1 Gm-c1066 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1066-3867 5' similar to TR:024023 024023 NEOXANTHIN CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available through: ResGen, Invitrogen Corp. South Memorial Parkway Huntsville, AL 35801 For further in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Shoemaker R/Public Soybean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Public Soybean EST Project
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BM085672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                                                                         148
18.0%;
ilarity 74.1%;
Conservative
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                                                                                                                                                                                              //note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: //note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from mRNA isolated from unexpanded leaves and the shoot tips of 2 week old seedling from the cultivar Williams. The 2 week old seedlings were salt stressed in a solution of 500mM NaCl for 3 days prior to harvesting. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-xhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (800)-533-4363
                                                                                                                                                         Ø
                                                                                                                                                                                 Shoemaker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Leaf and shoot tip, salt stressed, 2 week
old seedling"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="SOYBEAN CLONE ID: Gm-c1066-3867"
/clone_lib="Gm-c1066"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Glycine max"
/db_xref="taxon:3847"
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                                                                                                                                                                                                                                                                                                                                                                                                                           Glycine max Glycine max Elborophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                  This clone is available through: ResGen, Invitrogen Corp. South Memorial Parkway Huntsville, AL 35801 For further in call: (800)-533-4363 or contact: ccu@resgen.com web site: www.resgen.com
                                                                                            Contact: Shoemaker R/Public Soybean EST F
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
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old seedling"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    was constructed in the laboratory of Dr. Randy
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Clemson University
100 Jordan Hall, Clemson, SC 29634, U
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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http://www.genome.clemson.edu/orders/index.html
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/cultivar="TA496"
/db_xref="taxon:4081"
/clone="clEG11G7"
/clone=lib="tomato breaker fi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pBluescriptSKmCUadapt; Site_1: EcoR1; Site_2: XhoI; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."

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/dev_stage="breaker"
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

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1 Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
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/strain="TO1000DH3"
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/note="Vector: pHOS1; Site_1: BstXI; /genomic DNA inserted into pHOS1 using genomic DNA inserted 200 t
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               agacaaatacgccgaagattcatcgaacattaagtggattgatgctccagattgcttctg
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Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Chris Town
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            cdtown@tigr.org
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                                                                                                                                                                                                                                                           /organism="Brassica oleracea"
/strain="701000DH3"
/db_xref="raxon:3712"
/clone="BOHBT02"
/clone=1bb="BOHB"
/clone=1bb="BOHB"
/note="Vector: pHOS1; Site_1: 1
genomic DNA inserted into pHOS:
a 170 c 131 g 155 t
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Pred. No. 3.3e-82;
); Mismatches 137
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                                                                                                                                       Possible reversed clone: similarity on wrong strand This available through: ResGen, Invitrogen Corp. 2130 South McParkway Huntsville, AL 35801 For further information call >-533-4363 or contact via email: ccu@resgen.com High quality sequence stop: 423.
                                                                                                                                                                                                                                                                                     Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
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Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                  Public Soybean EST Project Unpublished (1999)
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                                                                                                                                                                                                                                       Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                Contact: Shoemaker R/Public Soybean
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                                                                                                                                                                                                                                                          Forest Park Parkway,
314 286 1800
314 286 1810
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl
/clone_lib="Gm-cl068"
/tissue_type="Leaf, drought stressed,
                                                                                                                          Location/Qualifiers
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      EST408190 tomato breaker fruit, clone cLEG35K8, mRNA sequence.
BE437072
BE437072.1 GI:9434915
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/lab_host="DH10B"
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                                                                        ATGATTTGCCTTACCATGTAAAAGGTAACACCCCACCGGCGATCTTAAAACAGAGGGTCGAT 420
                                                                                                                                                                                                                         CAAGGCTTATGCTGTTTTACGCTCGTGGGCTCTTCGGACTTGTTGATCACAGTAAAGGAA
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Lycopersicon esculentum

Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; eudicotyledons; Solanum;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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Alcala, J., Vrebalov, J., White, R., van der Hoeven, R.S., Holt, I.E., Liang, F., Hansen, T.S., Craven, M.B., Bowman, C.L., Ronning, C.M., Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBluescriptSKmCUadapt; Site_1: EcoR1; Site_2: XhOI; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."

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/lab_host="SOLR"
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/clone_lib="tomato breaker
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ggaaaacttcccgattccatcaaaggagtgtatgtgcgcaacggagctaacccacttcac 486
                                   ATTTCTGGGAATTTTGCTCCGGTACCGGAAAATCCAGTCTGTCAATCTCTTCCGGTCACC
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EST414153 tomato developing/immature green fruit Lycopersicon esculentum cDNA clone cLEM4F10, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l (bases 1 to 617)
Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Generation of ESTs from tomato fruit tissue, Unpublished (2000)
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Lycopersioon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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BE458861.1 GI:9503163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="fruit"
/dev_stage="immature green (5-35
/lab_host="SOLR"
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/clone="cLEM4F10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Lycopersicon esculentum"
/cultivar="TA496"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                                                                        16.9%;
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                                                                                                                                                                                                                                                     Score 303.4; DB 10;
Pred. No. 2.2e-79;
0; Mismatches 191;
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Search completed: July 24, 2002, 06:53:47 Job time: 5972 sec

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Minimum
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Perfect score:
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seq length:
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Maximum Match 100%
Listing first 45 summaries
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US-09-062-408-12
US-09-062-408-1-177
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PCT-US96-10986-4
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Patent No. 5225348
Sequence 1, Appli
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Sequence 12, Appli
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1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.8	1.8	1.8	1.8	1.8	1.8
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Sequence 12, Appl	Sequence 12, Appl	Sequence 14, Appl	Sequence 14, Appl	Sequence 448, App	Sequence 17, Appl	Sequence 17, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 25, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 33, Appl	Sequence 33, Appl	Sequence 33, Appl	Sequence 33, Appl	Sequence 14, Appl	Sequence 14, Appl

ALIGNMENTS

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Sequence 14, Application Patent No. 5670367
                                                                                                                                                                                           FILING DATE:

APPLICATION NUMBER: EP 91 114 300.6

FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 30472/114 IM

TELECOMMUNICATION INFORMATION:

TOTAL STAFF-9310
                                                                                                                                 TELEX: 899149
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT
NUMBER OF SEQUENCES: 52
 IMMEDIATE SOURCE:
CLONE: pTzgpt-
                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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ADDRESSEE: Foley & Lardner
                                                                                                                                 TELEFAX: (/-
TELEFAX: 899149
                                     STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                     TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 22313-0299
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FILING DATE: 08-DEC-1989
SEQ ID NO:3:
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; APPLICANT: HAGATA, SHIGEKAZU;SUGANO, SUMIO;KIM, DONG W.;
;UETSUKI, TAICHI;KAZIRO, YOSHITO
; TITLE OF INVENTION: DNA FRAGMENT AND EXPRESSION PLASMID;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONTAINING THE DNA FRAGMENT NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
                                                                                                                                              Sequence 1, Application US/08434881 Patent No. 5804376
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Best Local
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                                                                                                                               GENERAL INFORMATION:
                                                    APPLICANT: Braxton, Scott M.
APPLICANT: Wilde, Craig G.
APPLICANT: Diep, Dinh
TITLE OF INVENTION: Pancreas-Derived Serpin
NUMBER OF SEQUENCES: 2
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            ADDRESSEE: Incyte Pharmaceuticals, STREET: 3330 Hillview Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 4695
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Palo Alto
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RESULT 4
US-08-977-771-1/c
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US-08-434-881-1
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Best Local Similarity
                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Braxto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
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NAME/KEY:
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LENGTH: 1221 base pairs
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TELEPHONE: 415-855-0555
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                                                                                                                                                                                       APPLICANT: Wilde, Cr
APPLICANT: Diep, Din
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                             CITY: Palo Alto
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                                                                                           COUNTRY:
                                                                                                            STATE:
                                                                                                                                          STREET:
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Diep, Dinh
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                                                                                               USA
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   SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
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Pred. No. 0.51;
0; Mismatches 58;
    Version #1.30
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: CLASSIFICATION: FILING DATE:

08/ 434,881

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/977,771

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GENERAL INFORMATION:
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Best Local Similarity
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                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                     STREET: STREET: STREET: Palo Alto CITY: Palo Alto California
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                APPLICANT: Braxton, Scott M.
APPLICANT: Wilde, Craig G.
APPLICANT: Diep, Dinh
                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Pancreas-Derived Serpin
NUMBER OF SEQUENCES: 2
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LOCATION:
                                                                                                                                         COUNTRY: UZIP: 94304
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CLONE: 222689
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CLASSIFICATION:
                             APPLICATION NUMBER:
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                               US/09/361,773
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RESULT 6
US-09-026-408-12/c
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US-09-361-773-1
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Best Local Similarity
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APPLICANT: Ni et al.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/934,011
FILING DATE: 15-AUG-1997
                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,408
FILING DATE: Herewith
                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PANCREAS-DERIVED PLASMINOGEN ACTIVATOR TITLE OF INVENTION: INHIBITOR NUMBER OF SEQUENCES: 15
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APPLICATION NUMBER:
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REGISTRATION NUMBER: 339
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                         COUNTRY: USA
ZIP: 20005-3934
                                                                                                                                                                                                                                                           STREET: 1100 NEW CITY: WASHINGTON
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                                                  CLASSIFICATION:
                                                                                                                                                                                                                                             STATE:
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TYPE: nucleic acid
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Pred. No. 0.51;
0; Mismatches 58;
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US-09-026-408-1/c
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INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 1370 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09026408 Patent No. 6303338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 69; Conserv
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Best Local
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APPLICANT: Ni et al.
TITLE OF INVENTION:
TITLE OF INVENTION:
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NAME/KEY:
LOCATION:
                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,408
FILING DATE: Herewith
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                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 16-AUG-1996 ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157
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LOCATION:
                                                                                                                                                                                                                             ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 NEW YORK AVENUE, SUITE 600 CITY: WASHINGTON
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                                 CLASSIFICATION
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REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                               COUNTRY:
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                APPLICATION DATA:
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ilarity 54.3%;
Conservative
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67..1281
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121..1281
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67..120
 NUMBER:
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US 08/934,011
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Pred. No. 0.55;
0; Mismatches 58;
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US-08-991-789A-177
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GENERAL INFORMATION:
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Best Local Similarity
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TELEFAX: 202-371-2540
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FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
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LOCATION:
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REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1371 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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               SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,789A
                                                               ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BR PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP
                                                                                                                                                                                                                                                                                  Smith, John M. Reed, Steven G. TITLE OF INVENTION: COMPOS
                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                               CITY: Seattle
STATE: Washington
                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                 STREET: 701 Fifth Avenue,
FILING DATE:
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67..1242
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67..108
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16-AUG-1996
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   11-Dec-1997
                                                                                                                                                                                                                                                                  COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                                          IP Law Group

Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1488.0300002
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                                                   Version
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US-09-062-451-177

: Sequence 177, Application US/09062451

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ATTORNEY AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622,4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 788 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,451
FILING DATE: 04-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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STATE: Washin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 1.9%;
Local Similarity 48.2%;
nes 94; Conservative
                                                                                                                    CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 210121.419C3
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                                                                                                                                                                                                                                                                                                                                                                                                  Smith, John M.
Smith, John M.
Reed, Steven G.
Reed, Steven G.
NVENTION: COMPOSITIONS AND METHODS FOR THE
NVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                      6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Frudakis, Tony N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DESCRIPTION: SEQ ID NO: 177:
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                                        210121.419C2
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                                                       REFERENCE/DOCKET NUMBER: 0009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 559-6067
TELEFAX: (510) 559-5777
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1047 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
               MOLECULE TYPE:
                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Sequences for Production of TITLE OF INVENTION: 2,4-Diacetylphloroglucinol and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bangera, Mahalaxmi
APPLICANT: Weller, David M
APPLICANT: COOK, R. James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
HYPOTHETICAL:
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TYPE: nucleic acid
STRANDEDNESS: single
                              TOPOLOGY:
                                                                                                                                                                                        NAME: Connor, Margaret A REGISTRATION NUMBER: 300
                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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             DNA (genomic)
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RESULT 11

PCT-US96-10986-11/c
; Sequence 11, Application PC/TUS9610986
; GENERAL INFORMATION: Sequences for Production of
; TITLE OF INVENTION: 2,4-Diacetylphloroglucinol and Methods
; NUMBER OF SEQUENCES: 20
; NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: complement (1..1047); OTHER INFORMATION: /note= "phiD DNA sequence. SEQ ID; OTHER INFORMATION: NO:12 is translation (protein) of SUS-08-494-907-11
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                                                                                                                                REFERENCE/DOCKET NUMBER: A700
REFERENCE/DOCKET NUMBER: A700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (813) 289-2966
TELEPHAX: (813) 289-2967
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1047 base pairs
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephan A. Pendorf, DOMINIK & STEIN
STREET: 600 N. West Shore Boulevard, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE:
ORIGINAL SO
                                                                 TOPOLOGY: 11 MOLECULE TYPE:
                                ANTI-SENSE:
                                               HYPOTHETICAL:
                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Pendorf, Stephan A
REGISTRATION NUMBER: 326
                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                  ORIGINAL SOURCE:
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STREET: U.
TTTY: Tampa
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                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U
ZIP: 33609
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                                                                                                 STRANDEDNESS:
                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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Local Similarity 48.2%;
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Pseudomonas fluorescens
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                                                                   DNA (genomic)
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RESULT 12
525348-2
;Patest No. 5225348
;Patest No. 5225348
;Patest No. 5225348
;UETSKI, TAICHI: KASIRO, YOSHITO
; TILE OF INVENTION: DA FRAGMENT AND EX
;CONTAINING THE DNA FRAGMENT
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/447,823
; FILING DATE: 08-DEC-1989
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5225348-2
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; OTHER INFORMATION:
; OTHER INFORMATION:
PCT-US96-10986-11
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Best Local S
Matches 94
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Best Local Similarity
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NAME/KEY:
1317 ccacctttgggtcgc 1331
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                    520 gacggtatggttcac 534
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                                                                            gtgcgcaacggagctaacccacttcacgagccggtgacaggtcaccacttcttcgacgga 519
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                                                                                                                                                                                                                                                94;
                                                                                                                                                                                                                                                Conservative
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MMATION: /note= "phlD DNA sequence. SEQ
MMATION: NO:12 is translation (protein) o
                                                                                                                                                                                                                                                             1.98;
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                                                                                                                                                                                                                                              Score 33.4; DB 6; Length 1
Pred. No. 1.2;
0; Mismatches 101; Indels
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US-08-494-907-1/c

Sequence 1, Application US/08494907
Patent No. 5955298
GENERAL INFORMATION:
APPLICANT: Thomashow, Linda S
APPLICANT: Bangera, Mahalaxmi

밁 Q

Best Local Similarity 48.7 Matches 94; Conservative

48.28;

Pred. No. 1.9;
0; Mismatches 101;

Indels

0,

Gaps

0,

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OTHER INFORMATION:
OTHER INFORMATION:
US-08-494-907-1
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LENGTH: 3680 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (510) 559-6
TELEFAX: (510) 559-577
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                         FEATURE:
NAME/KEY:
LOCATION:
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TELECOMMUNICATION INFORMATION:
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NAME: Connor, Margaret A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Margaret A. Connor, USDA-ARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Weller, David M
APPLICANT: Cook, R. James
TITLE OF INVENTION: Sequences for Production of
TITLE OF INVENTION: 2,4-Diacetylphloroglucinol and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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                                                                                                         FEATURE:
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CITY: Albany
STATE: CA
                                                                      NAME/KEY:
                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: complement (2..1048)
OTHER INFORMATION: /note= "phil
OTHER INFORMATION: right to le
                                                                                                                                                                                                                                                                                          LOCATION: complement (1689..2855)
OTHER INFORMATION: /note= "phlC, transcribed from
OTHER INFORMATION: right to left"
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LOCATION: complement
OTHER INFORMATION: /r
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LOCATION: 2118..3371
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CLASSIFICATION: 435
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                                /note= "SEQ ID NO:1 contains genes
necessary for Phl synthesis."
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to right"
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right to left"
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/note= "phlB, transcribed from
right to left"
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/note= "phlA, transcribed from
right to left"
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Query Match

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Score 33.4;

DB 2;

Length 3680;

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PCT-US96-10986-1/c
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GENERAL INFORMATION:
TITLE OF INVENTION: Sequences for
TITLE OF INVENTION: 2,4-Diacetylp)
                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (813)289-2967
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                              MOLECULE TYPE: DNI
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Pseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF CORRESPONDENCE ADDRESS:
CORRESPONDENCE Stephan A. Pendorf, DOMINIK & STEIN
ADDRESSEE: Stephan A. Pendorf, DOMINIK & STEIN
CTRRET: 600 N. West Shore Boulevard, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
TOWN - Dendorf Stephan A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: A7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (813) 289-9966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                           FEATURE:
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LOCATION: complement (2889..3680)
OTHER INFORMATION: /note= "phla,
                                 OTHER INFORMATION: OTHER INFORMATION:
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TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC OPERATING SYSTEM:
 NAME/KEY:
                                                                     LOCATION:
                                                                                      NAME/KEY: misc_feature
                                                                                                                            OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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misc_feature
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                  complement (1210..1917)
MATION: /note= "phlB,
                                                                                                                                                                                                                  Pseudomonas fluorescens
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                                                                                                                        /note= "phlA, right to left"
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LOCATION: misc_feature; LOCATION: 1.3680
OTHER INFORMATION: /note=; OTHER INFORMATION: necessaper-us96-10986-1
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US-08-494-907-2/c
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Best Local S
Matches 94
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application Patent No. 5955298 GENERAL INFORMATION:
                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,907
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CONDOY, MATGARET A
REGISTRATION NUMBER: 30043
                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Thomashow, Linda S
APPLICANT: Bangera, Mahalaxmi
APPLICANT: Weller, David M
APPLICANT: Cook, R. James
                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Sequences for Production of TITLE OF INVENTION: 2,4-Diacetylphloroglucinol and Methods NUMBER OF SEQUENCES: 20
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les 94; Conservative
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INFORMATION: /note= "phlc,"
INFORMATION: right to left"
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2118..3371
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/note= "phlD, t
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to right"
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necessary for Phl synthesis."
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; NAME/KEY: misc_feature
; LOCATION: 1.5076
; OTHER INFORMATION: /note
; OTHER INFORMATION: invol
; OTHER INFORMATION: phl."
US-08-494-907-2
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5076 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 94; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEATURE:

NAME/KEY: misc_feature
LOCATION: 3514..4767
OTHER INFORMATION: /note
OTHER INFORMATION: to ri
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                                                                     2214
                                                                                                                                            2274
                                                                                                                                                                                                                 2334 GGCTAAACGGATGATTCAAAACACCCAAGTCAATGAACGGTATCTGGTCTTGCCCCATCGA 2275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 559-6067
TELEPAX: (510) 559-5777
TELEPAX: (510) 599-5777
NFORMATION FOR SEQ ID NO: 2:
2154 CATCCGGATGGTCGC 2140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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ORGANISM: Pseu
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                                                                                                                                                                                                                                    585 gactaaccggtttgttcaggaacgtcaattgggtcgaccggttttccccaaagccatcgg 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: complement (2..1270)
OTHER INFORMATION: /note= "phl
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OTHER INFORMATION: /note= "phlD, oTHER INFORMATION: right to left"
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LOCATION: complement (3085..4251)
OTHER INFORMATION: /note= "phlC, 1
OTHER INFORMATION: right to left"
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LOCATION: complement (2606...3313)
OTHER INFORMATION: right to left"
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LOCATION: complement (4285..5076)
OTHER INFORMATION: /note= "phla, to
OTHER INFORMATION: right to left"
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                                                                   CCGCATGTCTTCAATCGCCGCGCGCCAGGCCATTGAAAACGCGGGCTTGACCACGGACGA 2155
                                                                                                                                                           tgagetteaeggecaeaeeggtattgeeegaeteatgetattetaegeeagagetgeage 704
                                                                                         cggtatagtcgacccggcacacggaaccggtgtagctaacgccggttttggtctatttcaa 764
                                                                                                                                          TGAACTTGCGGTGCATACCGGCTTTACCCACCGCAGCATCGTGTATGAGCGAGAGGCTCG 2215
                            tggccggttattggc 779
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                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         right to left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "phlR, transcribed
to right"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "phlE,
                                                                                                                                                                                                                                                                                                                                                                                                               /note= "SEQ ID NO:2 contains genes involved in synthesis, activity, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0009.95
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Pred. No. 2.4;
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Search completed: July 24, 2002, 06:21:27 Job time: 8847 sec

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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM protein - protein search, using sw model
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2: sp_bacteria
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5: sp_nammal:*
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7: sp_mhc:*
8: sp_organel1
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
11: sp_rodent:
12: sp_virus:*
13: sp_vertebr
14: sp_unclass
15: sp_virus:*
16: sp_bacteri
17: sp_archeap
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Match Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is the number of results predicted by chance to have a ter than or equal to the score of the result being printed, ived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            July 19, 2002, 10:11:48; Search time 34.28 Seconds (without alignments) 3022.869 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-758-269-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MASFTATAAVSGRWLGGNHT......VPYGFHGTFIGADDLAKQVV 599
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       Q9M3Z9
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Q93ZU5
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                                                                                                                                     Q93zu5 arabidopsis
Q9m3z9 solanum tub
Q24023 lycopersico
Q9m9f5 arabidopsis
Q9fs24 vigna ungui
Q9m6e8 phaseolus v
Q9axz4 persea amer
Q9c6z1 arabidopsis
Q49505 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                               Description
                          Q9axz3
024592
021rm7
091rm7
049675
Q94ir2
                                                                                                                                                                                                                                                                                                                                                  Q91rr7 arabidopsis
4 persea amer
1 arabidopsis
5 arabidopsis
3 persea amer
2 zea mays (m
7 arabidopsis
5 arabidopsis
5 arabidopsis
2 phaseolus v
3 arabidopsis
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Q9yi25 ambystoma t	Q9YI25	13	533	6.9	216	45
mus	Q9ERN9	11	566	7.0	221	44
OMO	Q9NVH5	4	547	7.1	223	43
mus	Q9JJS6	1	566	٠	224	42
7	Q9HAY6	4	547		225	41
Q9ab98 caulobacter	Q9AB98	16	483	7.3	231	40
Q99nf1 mus musculu	Q99NF1	11	532	7.4	32.	39
O	Q9TXT9	ഗ	556	7.6	238.5	38
	Q90WH3	13	549		238.5	37
	Q9SHD9	10	618	7.7	244	36
Q9m079 arabidopsis	Q9M079	10	616		253	35
	Q90WH4	13	516	8.1	256	34
ω	Q91993	13	526		260	$\frac{\omega}{\omega}$
to	068868	N	342		270	32
	Q93VD5	10	552	9.6	302.5	31
	Q52008	N	490	9.6	303.5	30
P74370 synechocyst	P74370	16	480	10.1	317	29
ਰ	Q53353	N	485		352	28
	P74334	16	490		394	27
ū	005905	16	502	14.4	454.5	26
ಯ	Q9RK46	N	503	4٠	464	25
ū	006785	16	501	٠.	466	24
	Q93FA4	N	456	6.	N	23
Q9amil streptomyce	Q9AMI1	Ν	456	6.	527.5	22
Q9aa32 caulobacter	Q9AA32	16	483	6	N	21
	049895	10	446	ω	745	20
Q9axz5 persea amer	Q9AXZ5	10	524	5	798.5	19
4en8	4	10	200	26.6	w	18
065572 arabidopsis	065572	10	538	9.	937	17

ALIGNMENTS

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RESULT
Q9LRR7
Iuchi S., Kobayashi M., Shinozaki K.;
"Characterization of neoxanthin cleavag
thaliana.";
Submitted (APR-1999) to the EMBL/GenBan
EMBL; AB028617; BAB01336.1; -.
EMBL; AB026549; BAB70609.1; -.
InterPro; IPR004294; RPE65.
Pfam; PF03055; RPE65; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                Q9LRR7;
Q9LRR7;
Q1-QCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-QCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-DCT-2001 (TrEMBLrel. 19, Last annotation update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Q-CIS-EPOXYCAROTENOID DIOXYGENASE (NEOXANTHIN CLEAVAGE ENZYME).
Arabidopsis thaliana (Mouse-ear cres).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; endicots; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-COLUMBIA;
MEDLINE-20277480; PubMed-10819329;
                                                                                                                                     SEQUENCE FROM N.A. STRAIN=COL.;
                                                                                                                                                                      DNA Res. 7:131-135(2000).
[3]
                                                                                                                                                                                                                "Structural analysis of Arabidopsis thaliana chromosome 3. I. Se features of the regions of 4,504,864 bp covered by sixty Pl and
                                                                                                                                                                                                                                                                                                                           Sato S., Nakamura Y., Submitted (JUN-1999)
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to the EMBL/GenBank/DDBJ databases
                                                                         EMBL/GenBank/DDBJ databases
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Yamada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C. Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nayyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q93ZU5 PRELIMINARY; PRT; 599 AA. Q93ZU5; Q75ZU5; Q75ZU
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Best Local Similarity 71.3%;
Matches 432; Conservative
SEQUENCE FROM N.A. Serieve T.M., Jackson A., Thompson A., Taylor Burbidge A., Grieve T.M., Jackson A., Thompson A., Taylor "Structure and expression of a cDNA encoding a putative ne cleavage enzyme (NCE) isolated from a wilt-related tomato (Lycopersicon esculentum Mill.) library.";

J. Exp. Bot. 47:2111-2112(1997).
                                                                                                                                                                                                                   Lycopersicon esculentum (Tomato).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachec Spermatophyta; Magnollophyta; Eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TIEMBLIEL. 05, Created)
01-JUN-1998 (TIEMBLIEL. 06, Last sequence update)
01-DEC-2001 (TIEMBLIEL. 19, Last annotation update)
NINE-CIS-EPOXYCAROTENOID DIOXYGENASE.
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C Q9M9F5;
C Q1-CT-2000 (TrEMBLrel. 15, Created)
T Q1-CT-2000 (TrEMBLrel. 15, Last sequence update)
T Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
E F3F9.10.
S Arabidopsis thaliana (Mouse-ear cress).
Elkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracestophyta; Magnoliophyta; eudicotyledons; core eudicerosids II; Brassicales; Brassicaceae; Arabidopsis.
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Query Match
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EMBL; AC013430, AAF71797.1; -
EMBL; AC013430; GRAM_POS_ANCHORING; UNKNOWN_1.
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SEQUENCE FROM N.A.

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Buehler E., Johnson-Hopson C., Khan S., Kim C.,
Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Choi E., Conn L.,
Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J.

Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
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Local Similarity 67.7%;
nes 419; Conservative 8
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                                                                                                                  HIEVPDCFCFHLWNSWEEPETDEVVVIGSCMTPPDSIFNEHDETLQSVLSEIRLNLKTGE
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01-MAR-2001
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NEOXANTHIN C
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EMBL; AB030293; BAB11932.1; -.
SEQUENCE 612 AA; 67715 MW; E3
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MEDLINE=20317197; PubMed=10859185;
Tuchi S., Kobayashi M., Yamaguchi-Shinozaki K., Shinozaki K.;
"A stress-inducible gene for 9-cis-epoxycarotenoid dioxygenase
"A stress-inducible gene for 9-cis-epoxycarotenoid dioxygenase
involved in abscisic acid biosynthesis under water stress in dr
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                                            WIDAPDCFCFHLWNAWEEPETEEVVVIGSCMTPADSIFNECEESLKSVLSEIRLNLRTGK
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Pred. No. 3.2e
61; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phaseolus vulgaris (Kidney bean) (French bean).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids I; Falales; Fabaceae; Papilionoideae; Phaseoleae; Phaseol
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MEDLINE=20079657; Pubm
Qin X., Zeevaart J.A.;
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   421
                                         361
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                                                                                                                                             222
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                                                                                                                                                                                                                                                                                                            11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S-EPOXYCAROTENOID DIOXYGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                    9-cis-epoxycarotenoid cleavage reaction is the post abscisic acid biosynthesis in water-stressed Natl. Acad. Sci. U.S.A. 96:15354-15361(1999). AF190462; AAF26356.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYGFHGTFIGADDLAKQ
|||||||| : || ||
PYGFHGTFIHSKDLRKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GIARLMLEYARAAAGIVDPAHGTGVANAGLVYFNGRLLAMSEDDLPYQVQITPNGDLKTV
                                                                                                                                                                            HEPVTGHHFFDGDGMVHAVKFEHGSASYACRFTQTNRFVQERQLGRPVFPKAIGELHGHT
                                       GIARLLLFYARSLFQLVDGSHGMGVANAGLVYFNNHLLAMSEDDLPYHVRITSNGDLTTV
                                                                                                                                                                                                                    GFLVSHEKLHPLPKTADPSVQIAGNFAPVNEQPVRRNLPVVGKLPDSIKGVYVRNGANPL
                                                                                                                                                                                                                                               QYQPTSTSTTTTPTPIKPTTTTTTTPHRETKPLSDTKQPFPQKWNFLQKAAATGLDMVE
                                                                                                                                                                                                                                                                                        SNTWI--NTTLPSSCSSPFKDLASTSSSPTTLLPFKKRSSSNTNTITCSLQT---LHYPK 60
                                                                                                                                                                                                                                                                                                           SGRWLGGNHTQPPLSSSQSSDLSYCSS-----LPMASRVTRKLN-VSSALHTPPALHFPK 64
YEPVAGHHFFDGDGMVHAVKFTNGAASYACRFTETQRLAQEKSLGRPVFPKAIGELHGHS
                                                                                                                                                                                                         TALVSHESKHPLPKTADPKVQIAGNFAPVPEHAADQALPVVGKIPKCIDGVYVRNGANPL
                                                                                                                                                                                                                                                                                                                                 al Similarity
426; Conser
                                                                                                                                                                                                                                                                                                                                                                                  615
                                                                                                                                                                                                                                                                     SSNSPAIVVKPKAKE---
                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=10611388;
                                                                                                                                                                                                                                                                                                                                                                                  68075
                                                                                                                                                                                                                                                                                                                                         68.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                Score 2165; I
Pred. No. 6e-1
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  OCC10F862D7DE130 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               615
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95;
                                                                                                                                                                                                                                                            SNTKQ-----MNLFQRAAAAALDAAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                   regulatory
                                                                                                                                                                                                                                                                                                                                                     615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s; Rosidae;
Phaseolus.
                                                                                                                                                                                                                                                                                                                                36;
                                                                                                                                                                                                                                                                                                                               Gaps
                    461
                                                             401
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Q9AXZ4
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                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                 Chernys J., Zeevaart J.A.D.;

"Abscisic acid in avocado fruit.";

"Abscisic acid in avocado fruit.";

Submitted (JAN-2000) to the EMBL/GenBank/DDBJ

EMBL; AF224671; AAR00623.1; -.

InterPro; IPR000221; Protamine_P1.

PROSITE; PS00048; PROTAMINE_P1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O9AXZ4; PRELIMINARY; PRT; 625 AA. O9AXZ4; O1-JUN-2001 (TrEMBLrel. 17, Created) O1-JUN-2001 (TrEMBLrel. 17, Last sequence up O1-OCT-2001 (TrEMBLrel. 18, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Stro
Spermatophyta; Magnoliophyta;
NCBI_TaxID=3435;
                                                                                                                                                                                                                                                                                                                                                                    Dioxygenase.
SEQUENCE (
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CV. LULA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Persea americana (Avocado)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCED3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9-CIS-EPOXYCAROTENOID
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
          417
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                                                                                                                                                                                            142
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                                                                                                                                                                                                                                                                                              LPMASRVTRKLNVSSALHTPP---
                            ADPSVQIAGNEAPVNEQPVRRNLPVVGKLPDSIKGYYVRNGANPLHEPVTGHHFFDGDGM 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NSPATVVKPKAKESNTKQ-------MNLFQRAAAAALDAAEGFLVSH--EKLHPLPKT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YGFHGTFIGADDLAKQ
         EEPETDEVVVIGSCMTPPDSIFNESDENLKSVLSEIRLNLKTGESTRRPIISNEDQQVNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YGFHGTFIHSKDLRKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YGDNRYGGEPLFLPGEGGEEDEGYILCFVHDEKTWKSELQIVNAVSLEVEATVKLPSRVP 581
                                                                                                                              IVDPAHGTGVANAGLVYFNGRLLAMSEDDLPYQVQITPNGDLKTVGRFDFDGQLESTMIA
                                                                                                                                                                                                                                  LTPSIEKNPGSHQVKTDQSGPNRVGPNWNIFQRTAAFALDAIEEKLIARVLERRHPLPKT
                                                                                                                                                                                                                                                                           LPISKNLSRPKNFIMLKHNTPLIQCCSHSPSSSSAAVLHLPPKQPTKSKPSIKKGEKSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YGEEKFGGEPLFLP-NGEEEGDGYILAFVHDEKEWKSELQIVNAQNLKLEASIKLPSRVP
Similarity
                                                                                                                                                                                                                                                                                                                                                                    625
                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                    69724 MW;
                                                                                                                                                                                                                                                                                                                           65.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIOXYGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptophyta;
ta; Laurales;
                                                                                                                                                                                                                                                                                                                 Score 2066.5; DB 1
Pred. No. 4.4e-156;
4; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                    A56F33042D5F2CB6
                                                                                                                                                                                                                                                                                              Lauraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                                  93;
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                                                                                                                                                                                                                                                                                                                                                                    CRC64;
                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Persea
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RX MEDLINE=201016719; Pubmed=11130712;

RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA Mhite O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA White O., Alonso J., Altafi H., Araujo R., Cheu R.F., Chin C.W.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Fujii C.Y.,

RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

"Sequence and analysis of chromosome 1 of the plant Arabidopsis

"" **Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
9-CIS-EPOXYCAROTENOID DIOXYGENASE, PUTATIVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dioxygenase
SEQUENCE
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Local S
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                           DSIKGYYVRNGANPLHEPVTGHHFFDGDGMYHAVKFEHGSASYACRFTQTNRFVQERQLG
                                                                                                                                                NLFQRAAAAALDAAEGFLVSHEKLHPLPKTADPSVQIAGNFAPVNEQPVRRNLPVVGKLP
                                                                                                                                                                                                                                   SPSSSVSFTNTKPR----RRKLSANSVSDTPNLLNFPNYPSPNPII----PEKDTSRW
                                                                                                                                                                                                                                                                     SQSSDLSYCSSLPMASRVTRKLNVSSALHTPPALHFPKQSSNSPAIVVKPKAKESNTKQM
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DCIDGVYLRNGANPLFEPVSGHHLFDGDGMVHAVKITNGDASYSCRFTETERLVQEKQLG
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                                                                                                                 NPLQRAASAALDFAETALLRRERSKPLPKTVDPRHQISGNYAPVPEQSVKSSLSVDGKIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC074176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             408:816-820(2000).
AC074176; AAG50855.1;
                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65336 MW;
                                                                                                                                                                                                                                                                                                                                                                              64.9%;
                                                                                                                                                                                                                                                                                                                                                        69;
                                                                                                                                                                                                                                                                                                                                               Score 2044.5;
Pred. No. 2.3e
69; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6A79B2BF7EAA8179 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              589
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edons; core e
                                                                                                                                                                                                                                                                                                                                                  5; DB 10;
2.3e-154;
nes 101; I
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                                                                                                                                                                                                                                                                                                                                                     Gaps
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RESULT
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Query Match
Best Local s
Matches 380
                                                                    EU Arabidopsis sequencing pro
Submitted (MAR-2000) to the E
EMBL; AL021710; CAA16715.1; -
EMBL; AL161548; CAB78837.1; -
InterPro; IPR004294; RPE65.
Pfam; PF03055; RPE65; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  049505
049505;
01-JUN-1998
01-JUN-1998
                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
NEOXANTHIN CLEAVAGE ENZYME-LIKE PROTEIN.
                                                                                                                                                                             SEQUENCE FROM N.A.
Hilbert H., Braun M.,
Mewes H.W., Lemcke K.,
                                                                                                                                                                                                                                                                                                                                                                                                  F28J12.10 OR AT4G18350
                                                                                                                                                                                                                                Submitted
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                                                                                                                                              SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                    Bevan
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PYQVRVTDNGDLETIGRFDFDGQLSSAMIAHPKIDPVTKELFALSYDVVKKPYLKYFKFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVLSEIRLNLKTGESTRRPIISNEDQQVNLEAGMVNRNMLGRKTKFAYLALAEPWPKVSG
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G., Ridley P.,
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Hilbert H.,
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  Conservative
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to the E
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to the I
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            . 5%;
                                                          MW;
                                                                                                                                 proj
  82;
                                                                                                                                                                   r E., Brandt A., Du
r K.F.X.;
EMBL/GenBank/DDBJ
Score 1991; D
Pred. No. 4.1e
32; Mismatches
                                                                                                                                                                                                                              n S., Mewes H.W., I
EMBL/GenBank/DDBJ
                                                                                                                      EMBL/GenBank/DDBJ
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            1991;
No. 4.
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 DB 10;
1.1e-150;
nes 105;
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                       Length
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                                                                                                                                                                                                                                          Mayer
  22;
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 Gaps
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GGNHTQPPLSSSQSSDLSY--CSSLPMASRVTRKLNVSSALHTPPALHFPKQSSNSPAIV

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                                                                                                                      Query Match
Best Local S
Matches 373
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=CV. LULA;
Chernys J., Zeevaart J.A.D.;
"Abscisic acid biosynthesis in
Submitted (JAN-2000) to the EM
EMBL; AF224672; AAK00632.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9AXZ3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Str
Spermatophyta; Magnoliophyta;
                                                                                                                                                                                                                              Dioxygenase.
SEQUENCE 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9-CIS-EPOXYCAROTENOID
                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Persea americana (Avocado)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCED1
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                                                                RKLNVSSALHTPPALHFPK------
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AALDAAEGFLVSH--EKLHPLPKTADPSVQIAGNFAPVNEQPVRRNLPVVGKLPDSIKGV
                                                                                                                        373; Conservative
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                                                                                                                                                                                                                              569
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yta; Laurales;
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Last sequence up
Last annotation
                                                                                                                                                                                                                                                                                        in avocado fruit.";
EMBL/GenBank/DDBJ databases
                                                                                                                        Score 1977; D
Pred. No. 5.2e
76; Mismatches
                                                                                                                                                                                                                              CD12075EE9022461
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                                                                                                                        DB 10;
5.2e-149;
nes 97;
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Lauraceae; P
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Best Local
Matches 37
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01-JAN-1998
01-JAN-1998
01-DEC-2001
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Bukaryota; Viridiplantae; Streptophyta; Embryophyt
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Panicoideae; Andropogoneae; Zea.

NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                              VP14.
                                                                                                                                                                         Tan B.C., Schwartz S.H., Zeevaart J.A., McCarty D.R "Genetic control of abscisic acid biosynthesis in m Proc. Natl. Acad. Sci. U.S.A. 94:12235-12240(1997).
EMBL; U95953; AAB62181.1; --
                                                                                                                                                                                                                                                                                                                                           VIVIPAROUS-14.
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                                                                                                                                         InterPro; IPR004294; RPE65.
Pfam; PF03055; RPE65; 1.
SEQUENCE 604 AA; 65587 M
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Tan B.C., Schwartz S.H., Zeevaart
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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-KPKAKESNTKOMNLFQRAAAAALDA-AEGFLVS-HEKLHPLPKTADPSVQIAGNFAPVN
                                   PARSRARAS - - - - - NSVRFSPRAVSSVPPAECLQAPFHKPVADLPAPSRKPAATAVPGHA
                                                         PPLSSSQSSDLSYCSSLPMASRVTRKLNVSSALHTP---PALHFPKQSSNSPATVV----
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Gremblrel.
(Tremblrel.
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63.3%;
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Pred. No. 3.2e
73; Mismatches
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Last annotation updat
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No. 3.
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1.2e-145;
1es 122;
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a; Poales; Poaceae; PACC
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ID Q9
AC Q9
AC Q9
AC Q9
OT Q9
OT Q9
OT Q9
OS A A G9

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                                     Query Match
Best Local Similarity
Matches 323; Conser
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-OCT-2000 (TrEMBLrel. 15, Last annotation
9-CIS-EPOXYCAROTEMOLD DIOXYGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                     SEQUENCE !
                                                                                                                                                                           EMBL;
                                                                                                                                                                                              DNA
                                                                                                                                                                                                                                                                                                                                                                 STRAIN=COLUMBIA;
Sato S., Nakamura Y.,
Submitted (JUN-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9LRM7
                                                                                                                                                                                                                clones
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-COLUMBIA;
                                                                                                                                                                                                                                                                          Nakamura
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                                                                                                                                                                                                                                                    Structural
                                                                                                                                                                                                                                                                                          MEDLINE-20277480; PubMed=10819329;
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Pred. No. 5.2e-
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Cheuk R., Chen H., Kim C.J., Kc

Cheuk R., Carninci P., Dale J.

Bowser L., Carninci P.X., Jones T

Ishida J., Jiang P.X., Jones T

Lam B., Lee J.M., Li
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O49675;
O1-JUN-1998 (TrEMBLrel. 06, Created)
O1-JUN-1998 (TrEMBLrel. 06, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEOXANTHIN CLEAVAGE ENZYME-LIKE PROTEIN (AT4G19170/T18B16_140).
T18B16.140 OR AT4G19170.
                                                                                                                                                                                                                                                                  Benes V.,
Mayer K.F.
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Bevan M., Benes V., Re
Mewes H.W., Mayer K.,
Submitted (JAN-1998) t
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta,
Spermatophyta; Magnoliophyta; eudicotyledons; core «
eurosids II; Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                   EU Arabidopsis sequencing project; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
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                             Koesema E., Meyers M.C., Banh J., J.M., Goldsmith A.D., Hayashizaki T., Kamiya A., Karlin-Neumann G.,
         Kamiya A., K
J., Liu S.X.,
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EMBL; AL161550; CAB78019.1; --
EMBL; AY056789; AAL10480.1; --
InterPro; IPR004294; RPE65.
Pfam; PP03055; RPE65; 1.
SEQUENCE 595 AA; 65601 MW;
                                                                         Q94IR2 PRELIMINARY; PRT; 543 AA.
Q94IR2;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CARCTENOID 9,10-9',10' CLEAVAGE DIOXYGENASE.
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Satou N
           Phaseolus vulgaris (Kidney bean) (French bean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseol
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                                                                                                                                                                                                                                                                       TIGRYDFDGKLAMSMTAHPKTDPITGETFAFRYGPV-PPFLTYFRFDSAGKKQRDVPIFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TASVARGALTAARVLTGQYNPVNGIGLANTSLAFFSNRLFALGESDLPYAVRLTESGDIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TFIDP-----PSRPSVDPKHVLSDNFAPVLDELPPTDCEIIHGTLPLSLNGAYIRNGPNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GFLVSHEKLHPLPKTADPSVQIAGNFAPVNEQPVRRNLPVV-GKLPDSIKGVYVRNGANP 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRVTRKLNVSSALHTPPALHFPKQSSNSPAIVVKPKAKESNTKQMNLFQRAAAAALDAAE 10:
                                                                                                                                                                                                                                 S--LEVEATVKLPSRVPYGFHGTFIGADDLAK
                                                                                                                                                                                                                                                                                                                             LVTGIVRRHPISAR-----NLDFAVINPAFLGRCSRYVYAAIGDPMPKISGVVKLDVSKG
                                                                                                                                                                                                                                                                                                                                                                                               MTSPSFLHDFAITKRHAIFAEIQLGMRMNMLDLVLEGGSPVGTDNGKTPRLGVIPKYAGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QFLPRGPYHLFDGDGMLHAIKIHNGKATLCSRYVKTYKYNVEKQTGAPVMPNVFSGFNGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPITNPSDNNDRRNKPKTLH----NRTNHTLYSSPPKLRPEMTLATALF----TTVEDVIN
                                                                                                                                                                                                                   SPELEIVAAVRLPRRVPYGFHGLFVKESDLNK
                                                                                                                                                                                                                                                                                                   E----
                                                                                                                                                                                                                                                                                                                                                                                   ESEMKWFEVPGFNIIHAINAWDEDDGNSVVLIAPNIMSIEHTLERMD-LVHALVEKVKID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 36.7
10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai
Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                    -VKKHLYGDNRYGGEPLFLPGEGG----EEDEGYILCFVHDEKTWKSELQIVNAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 968;
No. 1.
                                                                                                                                                                                                                                             596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                          update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149
                                                                                                                                                                                                                                                                                                                                                                                 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Schwartz S.H., Qin X., Zeevaart J.A.D.;
"Characterization of a Novel Carotenoid Plants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (APR-2001) to the EMBL; AY029525; AAK38744.1; Dioxygenase.
 536
                      593
                                             476
                                                                                           416
                                                                                                                                                                435
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                                                                                                                                                                                                                                                                                                                                                                      V-YDKNKVARFGILDKYAEDSSNIKWIDAPDCFCFHLWNAWEEPETDEVVVIGSCMTPP-
                                                                                                                                                                                                                                                                                                                                                                                                                   NGAEGGLV---KVDPKPTNGFSSKVIDLLEKLLVKFLYDSSLPHHYLTGNFGPVTETPPT
DEDTO
                      DLAKQ
                                                         PGEGGEEDEGYILCFVHDEKTWKSELQIVNAVSLEVE--ATVKLPSRVPYGFHGTFIGAD
                                                                                         RYVYGTTLDSIAKUTGIIKFDLHAEPDHGKEKLEVGGNVQGLYDLGPGKEGSEAVYIPRV
                                                                                                                                                                                                                                                                              KILALSEADKPYAIKVFEDGDLQTLGMLDYDKRLGHSFTAHPKVDPFTGEMFSFGY-AHT
                                                                                                                                                                                                                                                                                             RLLAMSEDDLPYQVQITPNGDLKTVGRFDFDGQLESTMIAHPKVDPESGELFALSYDVVS
                                                                                                                                                                                                                                                                                                                           SRLKQEEYFGRSKFMK-IGDLKGLFGLLMVNIHMLRTKLKVLDLSYGGGTTNTALVYHHG
                                                                                                                 -DSI---FNESDENLKSVLSEIRLNLKTGESTRRPIISNEDQQVNLEAGMVNRNMLGRKT 490
                                                                                                                                                                                     FSFDSTKKARFGVLPRYAKDEQHIRWFELPNCFIFHNANAWE--EEDEVVLITCRLQNPK
                                                                                                                                                                                                                                  PPYITYRVISKDGYMHDPVPITISDPIMMHDFAITENYAVFMDLPLIFRPKEMVKNKTLI
                                                                                                                                                                                                                                                       KPYLKYFRFSPDGTKSPDVEIQLDQPTMMHDFAITENFVVVPDQQVVFKLPEMIRGGSPV 376
                                                                                                                                                                                                                                                                                                                                                NRFVQERQLGRPVFPKAIGELHGHTGIARLMLFYARAAAGIVDPAHGTGVANAGLVYFNG 256
                                            PGIESEEDDGYLVLFVHDENAGKSFVHVIDAKTMSADPVAVVELPNRVPYGFHAFFVTEE
                                                                                                                                       LDNVGGTVQEKLENFSNELYEMRFNMKTGEASQKKLSAS----TVDFPRVNENYTGRKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                      597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         543
 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61100 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 959.5; DB 1
Pred. No. 6.3e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F22C9883A05325F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cleavage Dioxygenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                           434
                                                                                                                                                                                                                                                                               242
                                                                                                                                                                                                                                                                                                                                                                                                                     64
                                                                                                                                                                                                                                  302
                                                                                                                                                                                                                                                                                                                           183
                                                                    592
                                                                                           475
                                                                                                                                       415
                                                                                                                                                                                    360
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Search completed: July 19, 2002, 10:15:43 Job time: 235 sec

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Minimum
Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Run
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pu and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB seq
2280.5
2280.5
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1991
1930
1930
1663.5
968
968
                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                                    3150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A_Geneseq_032802:*

1: /SIDS1/gcgdata/n

2: /SIDS1/gcgdata/n

4: /SIDS1/gcgdata/n

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100:0
72:4
68:8
63:2
61:3
61:3
52:8
30:7
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length: 2000000000
                                                                                                                                                                                                                                                                                                                        Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
2. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
3. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*
4. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*
5. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*
6. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*
7. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*
8. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1987.DAT:*
9. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:*
10. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:*
11. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
12. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
13. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*
14. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*
15. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*
16. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*
17. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*
18. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*
20. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1996.DAT:*
21. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
22. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
23. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
24. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
25. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
26. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
27. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
28. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
29. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          747574 segs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-758-269-6
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Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MASFTATAAVSGRWLGGNHT.....VPYGFHGTFIGADDLAKQVV 599
                                                                                                                                                                                                                                                                                                                        Length
595
595
595
595
                                                                                                                                                                                                                                                                                                                        DВ
                      AAE04789
AAE74789
AAE74787
AAE04787
AAE04782
AAE04788
AAE72309
AAE04783
AAE04783
                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           747574
                   Arabidopsis thalia
Zea mays neoxanthi
Neoxanthin cleavag
Arabidopsis thalia
Arabidopsis thalia
                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                 Neoxanthin cleavag
Vigna unguiculata
                                                                                                                                                                                                                                     Arabidopsis thalia
Lycopersicon escul
Neoxanthin cleavac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        printed,
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Cryptosporidium pa	AAB11732	21	1042		-	45
Human retinol bind	AAR44618	14	357	3.9	122.5	44
Portion of Cryptos	AAB11727	21	1721		N	43
μ.	AAB11737	21	1043		N	42
Amino acid sequenc	AAG62841	22	620		150	41
	AAU04291	22	620	4.8	150	40
Ö	ABB71747	22	620		150	39
Beta, Beta-caroten	AAY97315	21	529		185.5	38
Human RECAP polype	AAB68872	22	579			37
	AAU04294	22	556		207.5	36
retinol	AAR44617	14	533		209	35
Human protein sequ	AAB93458	22	539		209.5	34
RPE65.	AAB73955	22	533	6.7	210	S
0	AAB93108	22	547		223	32
-2,	AAU04292	22	532	7.4	232.5	31
Zebra-2, beta-caro	AAU04293	22	549		238.5	30
Beta, Beta-caroten	AAY97314	21	506		247	29
3	AAG62840	22	516		256	28
ys protein	AAG32794	21	152		259.5	27
ı, Beta-carc	AAY97311	21	526		260	26
mays	AAG32793	21	153		264.5	25
Zea mays protein f	AAG32792	21	166		272.5	24
11a	AAB99881	22	177	8.9	279	23
	AAE12065	22	596		307.5	22
	AAE12066	22	570	0.	322.5	21
\sim	AAB72307	22	446	Ψ	745	20
Arabidopsis thalia	AAG31335	21	431	ა	34.	19
æ	AAB72303	22	544	7.		18
ST	AAG13117	21	501	9.	25.	17
S	AAE04790	22	538	9.	w	16
S	AAE04785	22	538		938	15
ist	AAG13115	21	539	9	ω	14
is thal	AAG13116	21	538	9	w	13
Arabidopsis thalia	AAG31334	21	517	0	5	12

ALIGNMENTS

AAE04784 ID AAE(

AAE04784 standard; Protein;

599

B

AAE04784;

10-SEP-2001

(first entry)

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WPI; 2001-400081/43.
N-PSDB; AAD09396.
                                                                                    13-JAN-2000; 2000JP-0010056
11-JAN-2001; 2001JP-0003476
                                                                                                             11-JAN-2001; 2001EP-0300218
                                                                                                                                                                  Arabidopsis thaliana.
                                                                                                                                                                                           Neoxanthin cleavage enzyme; AtNCED3; abscisic acid; ABA; herbicide; stress tolerance; transgenic plant; plant breeding; antisense-therapy;
                                                                                                                                                                                                                     Arabidopsis thaliana neoxanthin cleavage enzyme, AtNCED3.
                                                  Iuchi S,
                                                                   (RIKE ) RIKEN KK.
                                                                                                                               18-JUL-2001.
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                                                  Shinozaki K;
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A DNA encoding a protein with a neoxanthin cleavage activity for producing transgenic plants with improved or decreased stress tolerance

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to neoxanthin cleavage enzymes and their corresponding cDNA molecules. Neoxanthin cleavage enzyme plays a key role in endogenous abscisic acid (ABA) biosynthesis under drought stress. Neoxanthin cleavage enzyme is used for improving stress tolerance in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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Local Similarity 100.0%;
hes 599; Conservative (
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                                                    EDEGYILCFVHDEKTWKSELQIVNAVSLEVEATVKLPSRVPYGFHGTFIGADDLAKQVV
                                                                                                    DPESGELFALSYDVVSKPYLKYFRFSPDGTKSPDVEIQLDQPTMMHDFAITENFVVVPDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tomato; neoxanthin cleavage enzyme; LeNCED1; abscisic acid; ABA; stress tolerance; transgenic plant; plant breeding; antisense-therapy; plant growth protectant; herbicide.
                                                                                                                                                                                                                                                                                                         Sequence
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11-JAN-2001;
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                                                                        LPKTADPSVQIAGNFAPVNEQPVRRNLPVVGKLPDSIKGVYVRNGANPLHEPVTGHHFFD 172
                                                                                                                                                                                                      TATAAVSGRWLGGNHTQPPLSSSQSSDLSYCS---SLPMASRVTRKLNVSSALHTPPALH 61
                                                       lpktadprvqisgnfapvpenpvcqslpvtgkipkcvqgvyvrnganplfeptaghhffd
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71.78;
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Pred. No. 4.4e
63; Mismatches
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                                                                                                                                                            Novel isolated defence-related signalling gene isolated from sunflower encoding neoxanthin cleavage enzyme, amino acid permease or glutamic acid-rich protein useful for increasing resistance of plant to a
                                                                                                                                                                                                                                                                                                                                     (PION-)
This invention relates to defence-related signalling genes isolated from the sunflower (Helianthus annums). The genes encode a neoxanthin cleavage enzyme (NCE), an amino acid permease (AAP) and a glutamic acid rich protein (GRP). The signalling gene is useful for increasing the
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23-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               resistance of a plant to a pathogen such as fungus, virus, bacterium, nematode or insect (e.g. European corn borer), preferably Sclerotinia spp., phoma spp., or Phompsis spp, by stably incorporating a construct containing the gene into the genome of the plant. The gene is useful for regulating gene expression in a plant, in response to a stimulus such as infection with a pathogen, damage from a pathogen, hydrogen peroxide, jasmonic acid, methyl jasmonate, salicylic acid, oxalic acid or expression of a gene encoding oxalic acid oxidase. The genes are also useful for stem-preferred regulation of gene expression in a plant. The genes are useful in agriculture, particularly in the present series are acid (ABA) metabolism and for modifying amino acid transport and content in plants. The present sequence represents a neoxanthin cleavage enzyme-like protein from Lycopersicon esculentum used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      characterisation of
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andlang
                                                       FLPGE---GGEEDEGYILCFVHDEKTWKSELQIVNAVSLEVEATVKLPSRVPYGFHGTFIG
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                                                                                                                                                                                                                                           NEVVVPDQQVVEKLPEMIRGGSPVVYDKNKVARFGILDKYAEDSSNIKWIDAPDCFCFHL
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Pred. No. 4.4e-222;
3; Mismatches 90;
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Best Local S
Matches 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         corresponding CDNA molecules. Neoxanthin Cleavage enzyme plays a key role in endogenous abscisic acid (ABA) biosynthesis under drought stress. Neoxanthin cleavage enzyme is used for improving stress tolerance in a plant when expressed in a plant cell. The invention also relates to methods for increasing or decreasing stress tolerance in a plant by introducing the DNA into the plant, and a transgenic plant into which a neoxanthin cleavage enzyme is introduced. The improvement of stress tolerance in plants is useful, for example in plant breeding. Neoxanthin cleavage enzyme genes are useful for producing transgenic plants. An arid then removing the weed by growing transformant weed for several years and then removing the weed by specifically lowering stress tolerance in the weed by inducing an inducible promoter. The present sequence is vigna unguiculata neoxanthin cleavage enzyme, CPRD65 (Cowbea Responsive to Dehydration) protein. CPRD65 gene is isolated from cowpea plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A DNA encoding a protein wit
producing transgenic plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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11-JAN-2001;
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DB; AAD09399.
TGIARLMLFYARAAAGIVDPAHGTGVANAGLVYFNGRLLAMSEDDLPYQVQITPNGDLKT
                                                                          LHEPVTGHFFFDGDGMVHAVKFEHGSASYACRFTQTNRFVQERQLGRPVFPKAIGELHGH
                                                                                                                                                \tt etalvsherkhplpktadprvqiagnfapvpehaadqglpvvgkipkcidgvyvrnganp
                                                                                                                                                                                EGFLVSHEKLHPLPKTADPSVQIAGNFAPVNEQPVRRNLPVVGKLPDSIKGVYVRNGANP
                                                                                                                                                                                                                                                                                                                                                           ssasntwfnatlpsppfkdlpsts-sptnllpl--rktsssntitcslqt---lhfpkqy
                                                                                                                                                                                                                                                                                                                                                                                                              AAVSGRWLGGNHTQPPLSSSQSSDLSYCSSLPMASRVTRKLN-VSSALHTPPALHFPKQ-
                                             1 yepvaghhffdgdgmvhavkftngaasyacrftetqrlsqekslgrpvfpkaigelhghdgdgmvhavkftngaasyacrftetqrlsqekslgrpvfpkaigelhghdgdgmvhavkftngaasyacrftetqrlsqekslgrpvfpkaigelhghdgdgmvhavkftngaasyacrftetqrlsqekslgrpvfpkaigelhghdgdgmvhavkftngaasyacrftetqrlsqekslgrpvfpkaigelhghdgdgmvhavkftngaasyacrftetqrlsqekslgrpvfpkaigelhghdgdgmvhavkftngaasyacrftetqrlsqekslgrpvfpkaigelhghdgdgmvhavkftngaasyacrftetqrlsqekslgrpvfpkaigelhghdgdgmvhavkftngaasyacrftetqrlsqekslgrpvfpkaigelhghdgdgmvhavkftngaasyacrftetqrlsqekslgrpvfpkaigelhghdgdgmvhavkftngaasyacrftetqrlsqekslgrpvfpkaigelhghdgdgmvhavkftngaasyacrftetqrlsqekslgrpvfpkaigelhghdgdgmvhavkftngaasyacrftetqrlsqekslgrpvfpkaigelhghdgdgmvhavkftngaasyacrftetqrlsqekslgrpvfpkaigelhghdgmyhdgdgmvhavkftngaasyacrftetqrlsqekslgrpvfpkaigelhghdgmyhdgdgmyhdgdgmyhdgaasyacrftetqrlsqekslgrpvfpkaigelhghdgmyhdgmyhdgaasyacrftetqrlsqekslgrpvfpkaigelhghdgmyhdgaasyacrftetqrlsqekslgrpvfpkaigelhghdgmyhdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdgaasyacrftetqrlsqehdg
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Pred. No. 1.1e
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h improved or decreased stress
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les 98;
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11-JAN-2001;
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DB; AAD09394.
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                                                                                                                                                                                                                                                                                              growth
                                                                                                                                                                                                                                                                                                      tolerance;
                                                                      Fig 10;
                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                       Kobayashi
                                                                                                                                                                                                                                                                                                                                 thaliana neoxanthin cleavage enzyme, AtNCED1
                                                                                                                                                                                           2000JP-0010056
2001JP-0003476
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                                                                      English.
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                                                                                                                                                        Shinozaki
                                                                                                                                                                                                                                                                                                      AtNCED1; abscisic acid; c plant; plant breeding;
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                                                                                                  a neoxanthin cleavage activity for ith improved or decreased stress to
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                                                                                                improved
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role in endogenous abscisic acid (ABA) biosynthesis under drought stress. Neoxanthin cleavage enzyme is used for improving stress tolerance in a plant when expressed in a plant cell. The invention also relates to methods for increasing or decreasing stress tolerance in a plant by introducing the DNA into the plant, and a transcariation also relates to

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neoxanthin cleavage enzymes and les. Neoxanthin cleavage enzyme

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                         Maize; neoxanthin cleavage enzyme; VP14; abscisic acid; ABA; herbicide; stress tolerance; transgenic plant; plant breeding; antisense-therapy;
                                                                                                                                 AAE04788
                                                                                                                                                            AAE04788 standard;
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                                                                                                                                                                                                                                                                                                                                                                PDSIFNESDENLKSVLSEIRLNLKTGESTRRPIISNEDQQVNLEAGMVNRNMLGRKTKFA 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGNHTQPPLSSSQSSDLSY--CSSLPMASRVTRKLNVSSALHTPPALHFPKQSSNSPAIV 73
                                                                                                                                                                                                                                               VHDEKTWKSELQIVNAVSLEVEATVKLPSRVPYGFHGTFIGADDLAKQV
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                                                                                                                                                                                                                               vhdeetkt selqiin avnlkleatiklps rvpygfhgtfvdsnelvdql\\
                                                                                                                                                                                                                                                                                        flaiaypwpkvsgfakvdlctgemkkyiyggekyggepfflpgnsgngeeneddgyifch
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                                                                                                                                                            Protein;
                                                                     cleavage
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                                                                      enzyme,
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Pred. No. 1e-192;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to neoxanthin cleavage enzymes and their corresponding cDNA molecules. Neoxanthin cleavage enzyme plays a key role in endogenous abscisic acid (ABA) biosynthesis under drought stress. Neoxanthin cleavage enzyme is used for improving stress tolerance in a plant when expressed in a plant cell. The invention also relates to methods for increasing or decreasing stress tolerance in a plant by introducing the DNA into the plant, and a transgenic plant into which a neoxanthin cleavage enzyme is introduced. The improvement of stress tolerance in plants is useful, for example in plant breeding. Neoxanthin cleavage enzyme genes are useful for producing transgenic plants. An arid and can be improved by growing transformant weed for several years and then removing the weed by specifically lowering stress tolerance in the weed by inducing an inducible promoter. The present sequence is Zea mays neoxanthin cleavage enzyme, VP14 protein related to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A DNA encoding a protein with a neoxanthin cleavage activity producing transgenic plants with improved or decreased stress
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11-JAN-2001;
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DB; AAD09400.
                                                      LVYFNGRLLAMSEDDLPYQVQITPNGDLKTVGRFDFDGQLESTMIAHPKVDPESGELFAL
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                                                                                      SYDVVSKPYLKYFRFSPDGTKSPDVEIQLDQPTMMHDFAITENFVVVPDQQVVFKLPEMI 370
                                                                                                                                                                      crftetarlrqeraigrpvfpkaigelhghsgiarlalfyaraacglvdpsagtgvanag
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                                                                                                                                                                                                                                             EQPVRRNLPVVGKLPDSIKGVYVRNGANPLHEPVTGHHFFDGDGMVHAVKFEHGSA-SYA 190
                                                                                                                                                                                                                                                                                                                   -KPKAKESNTKQMNLFQRAAAAALDA-AEGFLVS-HEKLHPLPKTADPSVQIAGNFAPVN 131
                                                                                                                                                                                                                                                                                                                                              parsraras----nsvrfspravssvppaeclqapfhkpvadlpapsrkpaaiavpgha
                                                                                                                                                                                                                                                                                                                                                                           PPLSSSQSSDLSYCSSLPMASRYTRKLNVSSALHTP---PALHFPKQSSNSPAIVV----
                                                                                                             {\tt lvyfngrllamseddlpyhvrvaddgdletvgrydfdgqlgcamiahpkldpatgelhal}
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2001JP-0003476
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                                                                                                                                                                                                                                                                                                                                                                                                      Score 1930; DB 22;
Pred. No. 1.7e-186;
3; Mismatches 122;
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RESULT
AAB72309
ID AAB7
                                                                                                     This invention relates to defence-related signalling genes isolated from the sunflower (Helianthus annuus). The genes encode a neoxanthin cleavage enzyme (NCE), an amino acid permease (AAP) and a glutamic acid rich protein (GRP). The signalling gene is useful for increasing the resistance of a plant to a pathogen such as fungus, virus, bacterium, nematode or insect (e.g. European corn borer), preferably incorporating a construct containing the gene into the genome of the plant. The gene is useful for regulating gene expression in a plant, in response to a stimulus such as infection with a pathogen, damage from a pathogen, hydrogen peroxide, jasmonic acid, methyl jasmonate, salicylic acid or expression of a gene encoding oxalic acid oxidase. The genes are also useful for stem-preferred regulation of gene expression in the plant. The genes are useful in agriculture, particularly in the
a plant. The genes are userul in agriculture, purchased and in the conditying abscisic acid (ABA) metabolism and for modifying amino acid transport content in plants. The present sequence represents a neoxanthin cleavenzyme-like protein from Zea mays used in the characterisation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated defence-related signalling gene isolated from sunflower encoding neoxanthin cleavage enzyme, amino acid permease or glutamic acid-rich protein useful for increasing resistance of plant to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
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23-MAY-2000;
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CURAGEN CORP.
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Best Local Sim
Matches 375;
                                                                                                                                    plant growth protectant
                                                                                                                                                Neoxanthin cleavage enzyme;
stress tolerance; transgeni
                                                                                                                                                                                                                                                     AAE04786 standard;
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           11-JAN-2001;
                     13-JAN-2000;
                                            11-JAN-2001;
                                                                                         EP1116794-A2
                                                                                                             Arabidopsis thaliana
                                                                                                                                                                                 Arabidopsis thaliana neoxanthin
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                                                                                                                                                                                                                                                                                                                                  ILCFVHDEKTWKSELQIVNAVSLEVEATVKLPSRVPYGFHGTFIGADDLAKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -KPKAKESNTKQMNLFQRAAAAALDA-AEGFLVS-HEKLHPLPKTADPSVQIAGNFAPVN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLSSSQSSDLSYCSSLPMASRVTRKLNVSSALHTP---PALHFPKQSSNSPAIVV----
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          2000JP-0010056
2001JP-0003476
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                                            2001EP-0300218
                                                                                                                                                 transgenic
                                                                                                                                                                                                                                                     Protein;
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                                                                                                                                                AtNCED5; abscisic acid; c plant; plant breeding;
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Pred. No. 1.7e-186;
3; Mismatches 122;
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SEQ IJ

NO:

37612

expression control;

pathway; promoter;

Claim

576 598

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The invention relates to neoxanthin cleavage enzymes and their CC corresponding cDNA molecules. Neoxanthin cleavage enzyme plays a key CC role in endogenous abscisic acid (ABA) biosynthesis under drought stress. CC Neoxanthin cleavage enzyme is used for improving stress tolerance in a cC plant when expressed in a plant cell. The invention also relates to comethods for increasing or decreasing stress tolerance in a plant by cintroducing the DNA into the plant, and a transgenic plant into which a cleavage enzyme is introduced. The improvement of stress cc tolerance in plants is useful, for example in plant breeding. Neoxanthin cleavage enzyme serial for producing transgenic plants. An arid cc cleavage enzyme genes are useful for producing transgenic plants. An arid claavage enzyme genes are useful for producing transgenic plants. An arid cc claavage enzyme genes are useful for producing stress tolerance in the cc weed by inducing an inducible promoter. The present sequence is cc Arabidopsis thaliana neoxanthin cleavage enzyme, AtNCED5 protein.

CC The AtNCED5 cDNA is obtained from an Arabidopsis plant-derived cDNA cc library using a cDNA of the CPRD65 (CowPea Responsive to Dehydration) cc gene isolated from cowpea plant as a probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Matcn
Best Local Similarity
Matches 323; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A DNA encoding a protein with a neoxanthin cleavage activity for producing transgenic plants with improved or decreased stress tolerance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAD09398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VGKLPDSIKGVYVRNGANPLHEPVTGHHFFDGDGMVHAVK--FEHGSASYACRFTQTNRF 199
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                                                                                                                                                                                   KNKVARFGILDKYAEDSSNIKWIDAPDCFCFHLWNAWEEPETDE----VVVIGSCMTPPD
                                                                                                                                                                                                                                                                                                                                                                                                      VQERQLGRPVFPKAIGELHGHTGIARLMLFYARAAAGIVDPAHGTGVANAGLVYFNGRLL
    aiadpwpkcsgiakvdiqngtvsefnygpsrfggepcfvpegegeedkgyvmgfvrdeek
                       ALAEPWPKVSGFAKVDLTTGEVKKHLYGDNRYGGEPLFLPGEGGEEDEGYILCFVHDEKT
                                                                                                   kekmarfgvlskqdltgsdinwvdvpdcfcfhlwnawee-rteegdpvivvigscmsppd
                                                                                                                                                                                                                                          LKYFRESPDGTKSPDVEIQLDQPTMMHDFAITENEVVVPDQQVVFKLPEMIRGGSPVVYD 379
                                                                                                                                                                                                                                                                                                                          AMSEDDLPYQVQITPNGDLKTVGRFDFDGQLESTMIAHPKVDPESGELFALSYDVVSKPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         llptktsprshllpqpknanisrrilinpfkiptlpdltspvpsp-----vklkptypn
                                                                              tifsesgeptrvelseirlnmrtkesnrkvivtg----vnleaghinrsyvgrksqfvyi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---lnllqklaatmldkiessivipmeqnrplpkptdpavqlsgnfapvnecpvqnglev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vgqipsclkgvyirnganpmfpplaghhlfdgdgmihavsigfdn-qvsyscrytktnrl 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fig 10; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kobayashi
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Pred. No. 1.8e-159;
)0; Mismatches 137; Ir
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33-COT-1999
34-OCT-1999
35-COT-1999
36-OCT-1999
31-OCT-1999
32-OCT-1999
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9908-0161359
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220;
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RESULT 10
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XX AABO47
AC AABO47
AC AABO47
XX Neoxan
KW Neoxan
KW Stress
KW Plant
COS Arabid
XX PD 18-JUL
XX 11-JAN
XX 11-JAN
XX 11-JAN
XX 11-JAN
XX WPI; 2
DR N-PSDB
XX WPI; 2
DR N-PSDB
XX WPI; 2
DR N-PSDB
XX ABOUC
XX ARABIC
XX 11-JAN
XX 11-J
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                                                                                                             A DNA encoding a protein with a neoxanthin cleavage activity for producing transgenic plants with improved or decreased stress to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neoxanthin cleavage enzyme; AtNCED2; stress tolerance; transgenic plant;
                              Example 10;
                                                                                                                                                                                                         N-PSDB; AAD09395
                                                                                                                                                                                                                                                                                                                                                   (RIKE ) RIKEN
                                                                                                                                                                                                                                                                                                                                                                                                             13-JAN-2000; 2000JP-0010056
11-JAN-2001; 2001JP-0003476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana neoxanthin cleavage enzyme, AtNCED2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-SEP-2001
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                           101pp; English
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                                                                                                                 improved or decreased stress tolerance
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plant breeding;
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RESULT 1 AAB72306

AAB72306 standard; Protein;

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AAB72306

16-MAY-2001

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to neoxanthin cleavage enzymes and their corresponding cDNA molecules. Neoxanthin cleavage enzyme plays a key crole in endogenous abscisic acid (ABA) biosynthesis under drought stress. Neoxanthin cleavage enzyme is used for improving stress tolerance in a plant when expressed in a plant cell. The invention also relates to methods for increasing or decreasing stress tolerance in a plant by commethods for increasing or decreasing stress tolerance in a plant by the DNA into the plant, and a transgenic plant into which a neoxanthin cleavage enzyme is introduced. The improvement of stress tolerance in plants is useful, for example in plant breeding. Neoxanthin cleavage enzyme genes are useful for producing transgenic plants. An arid cleavage enzyme genes are useful for producing transgenic plants. An arid cleavage enzyme genes are useful for producing transgenic plants. An arid cleavage enzyme the weed by growing transformant weed for several years and then removing the weed by specifically lowering stress tolerance in the weed by inducing an inducible promoter. The present sequence is arabidopsis thaliana neoxanthin cleavage enzyme, AtNCED2 protein.

The AtNCED2 cDNA is obtained from an Arabidopsis plant-derived cDNA library using a cDNA of the CRRD65 (CowPea Responsive to Dehydration) cleaves is solated from cowpea plant as a probe.
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Matches 210
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                     S--LEVEATVKLPSRVPYGFHGTFIGADDLAK 596
                                                                                                                   E----VKKHLYGDNRYGGEPLFLPGEGG----EEDEGYILCFVHDEKTWKSELQIVNAV
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speleivaavrlprrvpygfhglfvkesdlnk
                                                                                      \tt drddctvarrmygsgcyggepffvardpgnpeaeeddgyvvtyvhdevtgeskflvmdak
                                                                                                                                                                                   lvtgivrrhpisar----nldfavinpaflgrcsryvyaaigdpmpkisgvvkldvskg
                                                                                                                                                                                                                              LKTGESTRRPITSNEDQQVNLEAGMVNRNMLGRKTKFAYLALAEPWPKVSGFAKVDLTTG
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36.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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This invention relates to defence-related signalling genes isolated from Ct the sunflower (Helianthus annuus). The genes encode a neoxanthin cleavage CC enzyme (NCE), an amino acid permeases (AAP) and a glutamic acid rich CC protein (GRP). The signalling gene is useful for increasing the CC resistance of a plant to a pathogen such as fungus, virus, bacterium, CC nematode or insect (e.g. European corn borer), preferably incorporating a construct containing the gene into the genome of the plant. The gene is CC useful for regulating gene expression in a plant, in response to a stimulus such as infection with a pathogen, damage from a pathogen, CC hydrogen peroxide, jasmonic acid, methyl jasmonate, salicylic acid, coxalic acid or expression of a gene encoding oxalic acid oxidase. The genes are also useful for stem-preferred regulation of gene expression in a plant. The genes are useful in agriculture, particularly in the Dreeding of crop plants with improved agronomic traits, for modifying abscisic acid (ABA) metabolism and for modifying amino acid transport and content in plants. The present sequence represents a neoxanthin cleavage content is plants. The present sequence represents a neoxanthin cleavage
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                                                                                                                                                                                                                                                                                                                                                                               content in plants. enzyme-like protein characterisation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated defence-related signalling gene isolated from sunflower encoding neoxanthin cleavage enzyme, amino acid permease or glutamic acid-rich protein useful for increasing resistance of plant to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pathogen resistance; abscisic acid metabolism.
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23-MAY-2000;
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                   T-GIARLMLFYARAAAGIVDPAHGTGVANAGLVYFNGRLLAMSEDDLPYQVQITPNGDLK
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2000US-0206405.
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                                                                                                                                                                                                                                                                                                                                                                               sunflower NCE.
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Pred. No. 8.3e-89;
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                                                                                                                                                                                                                                                              Mismatches
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16-APR-1999
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30-APR-1999
31-AMY-1999
11-MAY-1999
11-MAY-1999
11-MAY-1999
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 25-FEB-2000; 2000EP-0301439
                                                       Arabidopsis thaliana
                                                                        hybridisation assay; genetic mapping; termination sequence.
                                                                                          Protein identification; signal transduction
                                                                                                                               17-OCT-2000
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                                     EP1033405-A2
                                                                                                           Arabidopsis thaliana protein fragment SEQ ID NO: 12489.
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                                                                                                                                                                                                                                                                                                                       gfniihainawdeddgnsvvliapnimsiehtlermd-lvhalvekvkidlvtgivrrhp
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Pred. No. 5.4e-88;
8; Mismatches 183
                                                                                 gene expression
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                                                                                 pathway; metabolic
expression control;
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S-0123180.
S-0123548.
S-0125788.
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S-0142977. S-0143542. S-0143624. S-0144005. S-0144085.

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                                  GDNRYGGEPLFLPGEGGEEDEGYILCFVHDEKTWKSELQIVNAVSLEVE--ATVKLPSRV
                 LEAGMVNRNMLGRKTKFAYLALAEPWPKVSGFAKVD----
          al Similarity 37.0
207; Conservative
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9908-0157753

9908-0157865

9908-0158232

9908-0158232

9908-0159294

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9908-0159330

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9908-0159331

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9908-0161350

9908-0161351

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9908-0161361

9908-0161361
                                                                                                                                                                                                                     29.8%;
37.0%;
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                                                                                                                                                                                                             Score 939; DB
Pred. No. 6.2e
06; Mismatches
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5.2e-86;
hes 198;
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hdaslplh----y
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112-JUL-1999
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RESULT 14
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21-APR 1999

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23-APR 1999

24-APR 1999

25-APR 1999

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21-MA
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21-SEP
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                                                                    Local Similarity
es 207; Conser
klsdgsiiisvhprpskgfssklldllerlvvklm-----
                                                                  29.8%; Silarity 37.0%; Poconservative 106;
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990S-0151065.
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990S-0149920.

990S-0149930.
                                                                Score 939; DB 21;
Pred. No. 6.2e-86;
6; Mismatches 198;
hdaslplh----y 48
                                                                                                Length 539;
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RESULT 1
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             A DNA encoding a protein with a neoxanthin cleavage activity for producing transgenic plants with improved or decreased stress tolerance
                                           WPI; 2001-400081/43.
N-PSDB; AAD09397.
                                                                                                                                                                                           Arabidopsis thaliana.
                                                                                                                                                                                                                      Neoxanthin cleavage enzyme; AtNCED4; abscisic acid; ABA; herbicide; stress tolerance; transgenic plant; plant breeding; antisense-therapy;
                                                                                                                                                                                                                                                 Arabidopsis thaliana neoxanthin cleavage enzyme, AtNCED4.
                                                                                                                                                                                                                                                                                                        AAE04785 standard; Protein;
                                                                      Iuchi S,
                                                                                         (RIKE ) RIKEN KK.
                                                                                                          13-JAN-2000;
11-JAN-2001;
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Example 10; Fig 10; 101pp; English.

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to neoxanthin cleavage enzymes and their corresponding cDNA molecules. Neoxanthin cleavage enzyme plays a key role in endogenous abscisic acid (ABA) biosynthesis under drought stress. Neoxanthin cleavage enzyme is used for improving stress tolerance in a plant when expressed in a plant cell. The invention also relates to methods for increasing or decreasing stress tolerance in a plant by introducing the DNA into the plant, and a transgenic plant into which a neoxanthin cleavage enzyme is introduced. The improvement of stress tolerance in plants is useful, for example in plant breeding. Neoxanthin cleavage enzyme growing transformant weed for several years and then removing the weed by specifically lowering stress tolerance in the weed by inducing an inducible promoter. The present sequence is a ransparathin cleavage enzyme is theliana neoxanthin plants enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thailana neoxanthin cleavage enzyme, AtNCED4 protein. The AtNCED4 cDNA is obtained from an Arabidopsis plant-derived cDNA library using a cDNA of the CPRD65 (CowPea Responsive to Dehydration) gene isolated from cowpea plant as a probe.
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                                                                                                                   GDNRYGGEPLFLPGEGGEEDEGYILCFVHDEKTWKSELQIVNAVSLEVE--ATVKLPSRV 580
                                                                                                                                                                              vdfprinecytgkkqryvygtildsiakvtgiikfdlhaeaetgkrmlevggnikgiydl 458
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Search completed: Job time: 45 sec

July 19, 2002, 10:11:42

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Copyright (c) 1993 - 2000 Compugen Ltd
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294 298 354 358	Qy 114 PKTADDSVQIAGNFAPVNEQPVERNLPVYGKLPDSIKGVVVRNGANPLHEPVTGHHFFDG	8 3 5 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	RESULT 1 T51936 T51936 T51936 C; Species: Solanum tuberosum (potato) C; Species: Solanum tuberosum (potato) C; Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_C: Accession: T51936 R; Burbidge, A.; Taylor, I.B.; Thompson, A. submitted to the EMBL Data Library, March 2000 A.; Description: Potato putative 9-cis-epoxycarotenoid diox A; Accession: T51936 A; Accession: T51936 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA A; Residues: 1-604 < BUR> A; Cross-references: EMBL:AJ276244; PIDN:CAB76920.1 C; Genetics: A; Gene: nced1	ALIGNMENTS	30 110.5 3.5 658 2 S60170 31 108 3.4 437 2 G77019 32 107.5 3.4 658 2 T39500 33 107 3.4 1461 2 T13157 34 107 3.4 26926 1 138344 35 106.5 3.4 1299 2 T47182 36 106 3.4 1299 2 T15968 37 106 3.4 3562 2 A47171 38 105.5 3.3 2591 2 T30288 39 105.5 3.3 2591 2 T30288 40 104.5 3.3 623 2 T52293 41 104.5 3.3 623 2 T52293 42 103.5 3.3 1080 2 A35088 43 103.5 3.3 375 2 B70449 44 103 3.3 375 2 B70449 44 103 3.3 4845 2 T31067
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414 NAWEEPETDEVVVIGSCMTPPDSIFNESDENLKSVLSEIRLNLKTGESTRRPIISNEDQQ 473

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nine-cis-epoxycarotenoid dioxygenase - tomato
N;Alternate names: probable neoxanthin cleavage enzyme
C;Species: Lycopersicon esculentum (tomato)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 20-Jun-2000
C;Accession: T07123
R;Burbidge, A.
Submitted to the EMBL Data Library, January 1998
A;Accession: T07123
A;Accession: T07123
A;Accession: T07123
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T07123
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A; Cross-references: EMBL: 297215;
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GLFGLVDHSKGTGVANAGLVYFNNRLLAMSEDDLPYHVKVTPTGDLKTEGRFDFDGQLKS
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                                                  GDGMVHAVKFEHGSASYACRFTQTNRFVQERQLGRPVFPKAIGELHGHTGIARLMLFYAR 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVNLEAGMVNRNKLGRKTEYAYLAIAEPWPKVSGFAKVNLFTGEVEKFIYGDNKYGGEPL
                                                                                                                                                                TMIAHPKLDPVSGELFALSYDVIQKPYLKYFRFSKNGEKSNDVEIPVEDPTMMHDFAITE
                                                                                                                                                                               TMIAHPKVDPESGELFALSYDVVSKPYLKYFRFSPDGTKSPDVEIQLDQPTMMHDFAITE
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Pred. No. 5.1
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r;Theologis, A; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, :
   Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cre
   ansen, N.F.; Hughes, B; Huizar, L.
   Nature 408, 816-820, 2010
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.;
   C.A.; Li, J.H.; Li, Y; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.;
   Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
   A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.
   ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
   A;Title: Sequence and analysis of chromosome 1 of the plant Arabidops
   A;Reference number: A86141; MUID:21016719
   A;Status: preliminary
   A.M.
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001
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A; Residues: 1-657 <S
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                                                       WIDAPDCFCFHLWNAWEEPETDEVVVIGSCMTPPDSIFNESDENLKSVLSEIRLNLKTGE 460
                                                                                                          QPTMIHDFAITENEVVIPDQQVVFRLPEMIRGGSPVVYDEKKKSRFGILNKNAKDASSIQ
                                                                                                                                                                                                    VGRFDFDGQLESTMIAHPKVDPESGELFALSYDVVSKPYLKYFRFSPDGTKSPDVEIQLD 340
                                                                                                                                                                                                                                                                                                                                                      LHEPVTGHHFFDGDGMVHAVKFEHGSASYACRFTQTNRFVQERQLGRPVFPKAIGELHGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MASFTATAAVSGRWL-----GGNHTQPPLSSSQSSDLSYCSSLP------MASRVT 45
                                                                                                                                          QPTMMHDFAITENFYVYPDQQVYFKLPEMIRGGSPVYYDKNKVARFGILDKYAEDSSNIK 400
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 STRRPIISNEDQQVNLEAGMVNRNMLGRKTKFAYLALAEPWPKVSGFAKVDLTTGEVKKH
                                      WIEVPDCFCFHLWNSWEEPETDEVVVIGSCMTPPDSIFNEHDETLQSVLSEIRLNLKTGE
                                                                                                                                                                                    SGRYDFDGQLKSTMIAHPKIDPETRELFALSYDVVSKPYLKYFRFTSDGEKSPDVEIPLD
                                                                                                                                                                                                                                                             LGIAKLMLFNTRGLFGLVDPTGGLGVANAGLVYFNGHLLAMSEDDLPYHVKVTQTGDLET
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67.7%;
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80; Mismatches
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ches 87;
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Maiti, R.; Marzia
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Dewar,
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probable 9-cis-epoxycarotenoid dioxygenase [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Datc: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: A86425 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Devansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000 Nature 408, 816-820, 2000 Nature 408, 816-820, 2000 Nature 408, 15, Li, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; C.A.; Li, J.H.; Li, Y.; Lil, X.; Liu, X.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Maiti, R.; Maithors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Rarzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Rithie: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719 A;Raccession: A86425 A;Raccession: A86425 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE005172; NID:g11094779; PIDN:AAG29711.1; GSPDB:GN00141 C;Genetics:
A;Map position: 1
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A86425
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A; Residues: 1-589 <STO>
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Best Local
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                                                                       GILDKYAEDSSNIKWIDAPDCFCFHLWNAWEEPETDEVVVIGSCMTPPDSIFNESDENLK 446
                                                                                                               PYQVQITPNGDLKTVGRFDFDGQLESTMIAHPKVDPESGELFALSYDVVSKPYLKYFRFS 326
                                                                                                                                                                                                                                                                                                                                                                                                                            SQSSDLSYCSSLPMASRVTRKLNVSSALHTPPALHFPKQSSNSPAIVVKPKAKESNTKQM 86
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 SVLSEIRLNLKTGKSTRRTIIPG-SVQMNLEAGMVNRNLLGRKTRYAYLAIAEPWPKVSG
                                                                                                                                                                                                                                                 RPVFPKAIGELHGHTGIARLMLFYARAAAGIVDPAHGTGVANAGLVYFNGRLLAMSEDDL
                                                                                                                                                                                                                                                                                          DCIDGVYLRNGANPLFEPVSGHHLFDGDGMVHAVKITNGDASYSCRFTETERLVQEKQLG
                                                                                                                                                                                                                                                                                                        DSIKGVYVRNGANPLHEPVTGHHFFDGDGMVHAVKFEHGSASYACRFTQTNRFVQERQLG
                                                                                                                                                                                                                                                                                                                                                                  NLFQRAAAAALDAAEGFLVSHEKLHPLPKTADPSVQIAGNFAPVNEQPVRRNLPVVGKLP 146
                           SVLSEIRLNLKTGESTRRPIISNEDQQVNLEAGMVNRNMLGRKTKFAYLALAEPWPKVSG
                                                        GILPRNAKDASEMVWVESPETFCFHLWNAWESPETDEVVVVIGSCMTPADSIFNECDEQLN
                                                                                                                                                                          PYQVRVTDNGDLETIGRFDFDGQLSSAMIAHPKIDPVTKELFALSYDVVKKPYLKYFKFS
                                                                                                                                                                                                                                  SPIFPKAIGELHGHSGIARLMLFYARGLFGLLNHKNGTGVANAGLVYFHDRLLAMSEDDL
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68.1%;
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Pred. No. 4.1e-147;
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Maiti, R.; M
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A; Note: F28J12.10;
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A; Residues: 1-377 <BEW>
A; Cross-references: EMB
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ADSIFNERDESLRSVLSEIRINLRTRKTTRRSLLVNED--VNLEIGMVNRNRLGRKTRFA
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64.5%;
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A;Molecule type: DNA
A;Residues: 1-583 <BEV>
A;Residues: 1-583 <BEV>
A;Cross-references: EMBL:AL021710
A;Experimental source: cultivar Columbia; BAC clone F28J12
A;Experimental source: rilivar Columbia; BAC clone F28J12
A;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, submitted to the Protein Sequence Database, February 1999
A;Reference number: Z15390
A;Accession: T04937 C;Accession: T04531; T04937
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Bran submitted to the Protein Sequence Database, February A;Reference number: Z15377
A;Accession: T04531 nine-cis-epoxycarotemoid dioxygenase homolog F28U12.10 - Arabidopsis thalia N;Alternate names: hypothetical protein T9A21.200 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999 597 E.; Brandt, 1998 A . ; Arabidopsis thaliana Ι.; Duesterhoeft, Mewes, H.W.; Α., Mayer, Bancro

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82; Mismatches 105; Score 1991; DB 2; Pred. No. 4.7e-143; Length 583; Indels 22; Gaps 6

SVRRNLTVEGTIPDCIDGYYIRNGANPMFEPTAGHHLFDGDGMVHAVKITNGSASYACRF 176 GGNHTQPPLSSSQSSDLSY--CSSLPMASRVTRKLNVSSALHTPPALHFPKQSSNSPAIV 73 PDSIFNESDENLKSVLSEIRLNLKTGESTRRPIISNEDQQVNLEAGMVNRNMLGRKTKFA 493 VVSKPYLKYFRFSPDGTKSPDVEIQLDQPTMMHDEAITENFVVVPDQQVVFKLPEMIRGG FNGRLLAMSEDDLPYQVQITPNGDLKTVGRPDFDGQLESTMIAHPKVDPESGELFALSYD 313 PVRRNLPVVGKLPDSIKGVYVRNGANPLHEPVTGHHFFDGDGMVHAVKFEHGSASYACRF 193 VKPKAKESNTKOMNLFQRAAAAALDAAEGFLVSHEKLHPLPKTADPSVQIAGNFAPVNEQ 133 SPVYYDKNKVAREGILDKYAEDSSNIKWIDAPDCFCFHLWNAWEEPETDEVVVIGSCMTP 433 FNNRLLAMSEDDLPYQLKITQTGDLQTVGRYDFDGQLKSAMIAHPKLDPVTKELHALSYD TKTERLVQEKRLGRPVFPKAIGELHGHSGIARLMLFYARGLCGLINNQNGVGVANAGLVY TQTNREVQERQLGRPVFPKAIGELHGHTGIARLMLFYARAAAGIVDPAHGTGVANAGLVY 253 GGIKTWP----QAQIDLGFRPIKRQPKVIKCTVQIDVTE-LTKKRQLFTPRTTATPP---SPVVFDGEKVSRLGIMPKDATEASQIIWVNSPETFCFHLWNAWESPETEEIVVIGSCMSP VVKKPYLKYFRFSPDGVKSPELEIPLETPTMIHDFAITENFVVIPDQQVVFKLGEMISGK 356 -----QHNPLRLNIFQKAAAIAIDAAERALISHEQDSPLPKTADPRVQIAGNYSPVPES 116 236 416 373 296 62

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A;Gene: vp14
A;Map position: 1
C;Function:
A;Description: catalyzes
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A;Residues: 1-604 <TAN>
A;Cross-references: EMBL:U95953; NID:g2232016; PIDN:AAB62181.1; PID:g2232017
A;Experimental source: strain W22
C;Genetics:
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C;Species: 2ea mays (maize)
C;Date: 23-Apr-1999 #sequence_revision
C;Accession: T04351
R;Tan, B.C.; McCarty, D.R.
submitted to the EMBL Data Library, Mar
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A; Accession: T04351
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RYAYLAVAEPWPKESGFAKEDLSTGELTKFEYGEGRFGGEPCFVPMDPAAAHPRGEDDGY
            MTPPDSIFNESDENLKSVLSEIRLNLKTGESTRRPIISNEDQQVNLEAGMVNRNMLGRKT
                                                                                                                                                      SYDVIKRPYLKYFYFRPDGTKSDDVEIPLEQPTMIHDFAITENFVVVPDHQVVFKLQEML
                                                                                                                                                                                SYDVVSKPYLKYFRFSPDGTKSPDVEIQLDQPTMMHDFAITENFVVVPDQQVVFKLPEMI
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                                                                                                                                                                                                                                                                                                             ERPPVHELPVSGRIPPFIDGVYARNGANPCFDPVAGHHLEDGDGMVHALRIRNGAAESYA
                                                                                                                                                                                                                                                                                                                            EQPVRRNLPVVGKLPDSIKGVYVRNGANPLHEPVTGHHFFDGDGMVHAVKFEHGSA-SYA 190
                                                                                                                                                                                                                                                                                                                                                                  AAPRKAEGGKKQLNLFQRAAAAALDAFEEGFVANVLERPHGLPSTADPAVQIAGNFAPVG
                                                                                                                                                                                                                                                                                                                                                                               -KPKAKESNTKQMNLFQRAAAAALDA-AEGFLVS-HEKLHPLPKTADPSVQIAGNFAPVN 131
                                                                                                                                                                                                                                                                                                                                                                                                                    PARSRARAS-----NSVRFSPRAVSSVPPAECLQAPFHKPVADLPAPSRKPAAIAVPGHA
                                                                                                                                                                                                                                                                                                                                                                                                                                            PPLSSSQSSDLSYCSSLPMASRVTRKLNVSSALHTP---PALHFPKQSSNSPAIVV----
                                                                                                                                                                                                          LVYFNGRLLAMSEDDLPYHVRVADDGDLETVGRYDFDGQLGCAMIAHPKLDPATGELHAL
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63.3%;
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Pred. No. 2.1e
73; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-Apr-1999 #text_change 08-Oct-1999
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hypothetical protein T18B16.140 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Decies: Arabidopsis thaliana (mouse-ear cress) C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999 C;Accession: T04438
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A; Map position: 4
A; Note: T18B16.140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-595 <BEV>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the Protein
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TASVARGALTAARVLTGQYNPVNGIGLANTSLAFFSNRLFALGESDLPYAVRLTESGDIE
                                                                                                                                                                                                                                                                           TVGRFDFDGQLESTMIAHPKVDPESGELFALSYDVVSKPYLKYFRFSPDGTKSPDVEI-Q
                                                                                                                                                                                                                                                                                                                                                                                                          T-GIARLMLFYARAAAGIVDPAHGTGVANAGLVYFNGRLLAMSEDDLPYQVQITPNGDLK 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GFLVSHEKLHPLPKTADPSVQIAGNFAPVNEQPVRRNLPVV-GKLPDSIKGVYVRNGANP 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRVTRKLNVSSALHTPPALHFPKQSSNSPAIVVKPKAKESNTKQMNLFQRAAAAALDAAE 101
SPELEIVAAVRLPRRVPYGFHGLFVKESDLNK
                            S--LEVEATVKLPSRVPYGFHGTFIGADDLAK
                                                                                          E-----VKKHLYGDNRYGGEPLFLPGEGG----EEDEGYILCFVHDEKTWKSELQIVNAV 566
                                                                                                                             LYTGIYRRHPISAR-----NLDFAYINPAFLGRCSRYYYAAIGDPMPKISGVVKLDVSKG
                                                                                                                                                         LKTGESTRRPIISNEDQQVNLEAGMVNRNMLGRKTKFAYLALAEPWPKVSGFAKVDLTTG 515
                                                                                                                                                                                                                                                                                                                          TIGRYDFDGKLAMSMTAHPKTDPITGETFAFRYGPV-PPFLTYFRFDSAGKKQRDVPIFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     QFLPRGPYHLFDGDGMLHAIKIHNGKATLCSRYVKTYKYNVEKQTGAPVMPNVFSGFNGV 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LHEPVTGHHFFDGDGMVHAVKFEHGSASYACRFTQTNRFVQERQLGRPVFPKAIGELHGH 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TFIDP-----PSRPSVDPKHVLSDNFAPVLDELPPTDCEIIHGTLPLSLNGAYIRNGPNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPITNPSDNNDRRNKPKTLH----NRTNHTLVSSPPKLRPEMTLATALF----TTVEDVIN
                                                             DRDDCTVARRMYGSGCYGGEPFFVARDPGNPEAEEDDGYVVTYVHDEVTGESKFLVMDAK
                                                                                                                                                                                           ESEMKWFEVPGFNIIHAINAWDEDDGNSVVLIAPNIMSIEHTLERMD-LVHALVEKVKID
                                                                                                                                                                                                                          SSNIKWIDAPDCFCFHLWNAWEEPETDEVVVIGSCMTPPDSIFNESDENLKSVLSEIRLN 455
                                                                                                                                                                                                                                                         {\tt MTSPSFLHDFAITKRHAIFAEIQLGMRMNMLDLVLEGGSPVGTDNGKTPRLGVIPKYAGD}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210;
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36.7%;
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Pred. No. 2.3e-65;
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Database,
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594
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April 1998
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RESULT T49193

neoxanthin cleavage N;Alternate names: p

protein

ncl - Arabidopsis MAA21.150

thaliana

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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: T49193
R;Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemc submitted to the Protein Sequence Database, April 2000
A;Reference number: 225018
A;Accession: T49193
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-538 <AIE>
A;Cross-references: EMBL:AL163818; GSPDB:GN00061; ATSP:MAA21.150
A;Experimental source: cultivar Columbia; BAC clone MAA21
C;Genetics:
A;Gene: ATSP:MAA21.150
A;Map position: 3
A;Introns: 72/3; 96/2; 101/2; 138/3; 172/1; 193/1; 230/1; 291/3; 338/1; 377/2; 411/
RESULT
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Best Local Similarity
Matches 207; Conserv
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                                                                                                                                                                                                  PYGFHALFVTEEQLQEQTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IKDGKATYVSRYVKTSRLKQEEFFGAAKFMK-IGDLKGFFGLLMVNVQQLRTKLKILDNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IAGNFAPV-NEQPVRRNLPVVGKLPDSIKGVYVRNGANPLHEPVTGHHFFDGDGMVHAVK 181 ::|||||: :| :|| | |: | :|:|||||: | :
                                                                                                                                                                                                                                   PYGFHGTFIGADDLAKQVV
                                                                                                                                                                                                                                                                   GEGRYGSEAIYVPRETAEEDDGYLIFFVHDENTGKSCVTVIDAKTMSAEPVAVVELPHRV
                                                                                                                                                                                                                                                                                               GDNRYGGEPLFLPGEGGEEDEGYILCFVHDEKTWKSELQIVNAVSLEVE--ATVKLPSRV
                                                                                                                                                                                                                                                                                                                                   VDFPRINECYTGKKQRYVYGTILDSIAKVTGIIKFDLHAEAETGKRMLEVGGNIKGIYDL
                                                                                                                                                                                                                                                                                                                                                                LEAGMVNRNMLGRKTKFAYLALAEPWPKVSGFAKVD-------LTTGEVKKHLY--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YGNGTANTALVYHHGKLLALQEADKPYVIKVLEDGDLQTLGIIDYDKRLTHSFTAHPKVD
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                                                                                                                                                                                                                                                                                                                                                                                                EDEVVLITCRLENPDLDMVSGKVKEKLENFGNELYEMRFNMKTGSASQKKLSASA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                     599
                                                                                                                                                                                                      537
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                 Arabidopsis
                                                                                  #text_change
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                 thaliana
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                                                                                  18-Aug-2000
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                 suspension
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                 cult
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A; Note: Anabaena sp. (strain PCC 7120)
C; Date: 14-Dec-2001 #sequence_revision
C; Accession: AG1944
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.;
Nakazaki, N.; Shimpo, S.; Sugimoto, M.

Sugimoto, M.;

Kuritz, T.; Sasamoto,
; Takazawa, M.; Yamada

Yamada,

S.; Watanabe, , M.; Yasuda,

Χ. Α.,

; Irigu Tabata

Cyanobacterium

is a synonym of Nostoc sp. strain PC 14-Dec-2001 #text_change 11-Jan-2002

PCC

7120

Anabaena sp.

(strain

PCC 7120)

hypothetical protein all1106 [imported] - C:Species: Anabaena sp.

10

DЬ δ 밁 δÃ DЬ Qγ Дd Qy В QΥ В

A; Molecule type: DNA A; Residues: 1.475 <KUR> A; Cross-references: GB:BA000019; A; Experimental source: strain PCC

SS

PIDN:BAB73063.1; C 7120

PID:g17130452;

GSPDB:GN00179

A; Reference number: AB1807; A; Accession: AG1944

Sequence of the Filamentous Nitrogen-fixing 7; MUID:21595285; PMID:11759840

A; Status: preliminary

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A;Cross-references: EMBL:AJ005813; PIDN:CAA06712 A;Experimental source: cultivar Landsberg erecta C;Genetics:
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A; Status: preliminary; t
A; Molecule type: mRNA
A; Residues: 1-538 <NEI>
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Best Local S
Matches 207
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                          PYGFHGTFIGADDLAKQVV
                                                                                             GDNRYGGEPLFLPGEGGEEDEGYILCFVHDEKTWKSELQIVNAVSLEVE--ATVKLPSRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IAGNFAPV-NEQPYRRNLPVVGKLPDSIKGVYVRNGANPLHEPVTGHHEFDGDGMVHAVK 181
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                                                                        GEGRYGSEAIYVPRETAEEDDGYLIFFVHDENTGKSCVTVIDAKTMSAEPVAVVELPHRV
                                                                                                                                                                       LEAGMYNRNMLGRKTKFAYLALAEPWPKVSGFAKVD------LTTGEVKKHLY--
                                                                                                                                                                                                                     EDEVVLITCRLENPDLDMVSGKVKEKLENFGNELYEMRFNMKTGSASQKKLSASA----
                                                                                                                                                                                                                                                        TDEVVVIGSCMTPPD-----SIFNESDENLKSVLSEIRLNLKTGESTRRPIISNEDQQVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IKDGKATYVSRYVKTSRLKQEEFFGAAKFMK-IGDLKGFFGLLMVNIQQLRTKLKILDNT 166
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PYGFHALFYTEEQLQEQTL
                                                                                                                                               VDFPRINECYTGKKQRYVYGTILDSIAKVTGIIKFDLHAEAETGKRMLEVGGNIKGIYDL
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Pred. No. 4.5e-63;
5; Mismatches 199;
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hypothetical protein - apple tree
C;Species: Malus domestica (apple tree)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
C;Accession: T17019
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T17019
                                                                            QY
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                                                                                                                                                                                                                                                                       A; Title: Apple messenger RNAs related to bacterial A; Reference number: 218655; MUID: 98179104 A; Accession: T17019
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                                                                                                                                                                                                                                                                                                                     R; Watillon, B.; Kettmann, R.; Arredouani, A.; Hecquet, J.; Plant Mol. Biol. 36, 909-915, 1998
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A; Gene: all1106
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                                            ESTMIAHPKVDPESGELFALSYDVVSKPYLKYFRFSPDGTKSPDVEI-QLDQPTMMHDFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSEAVFVPRPGATVEDDGWLITYVYDTGEESSELVVINAQDINSEPIARVLLPQRVPYGF
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--DDVASEFPRINENFLGQPTQYGYTSRLAKGSIPLFEGLIKYDLSNAKSQNYEYGQGRY
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                                                                                                                            Similarity
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                                                                                                             Score 745; DB 2;
Pred. No. 1.3e-48;
6; Mismatches 129
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Pred. No. 1.3e-48;
1; Mismatches 171;
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R.Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: E87345
A;Status: preliminary
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C;Genetics:
A;Gene: CC0776
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A; Residues: 1-483 <STO>
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LKSVLSEI----RLNLKTGESTRRPIISNEDQQVNLEAGMVNRNMLGRKTKFAYLALAEP-
                                      GEPRWFEAEPTYVLHWLNAYE--DGDEVVLDGYFQEKPIPRPLEGAPDGHGHLMAYLDEH
                                                                           SNIKWIDAPDCFCFHLWNAWEEPETDEVVVIGSCMTPP--
                                                                                                                    VPLPGPRLPHDMAFSSKYAILNDLPVFWDQELMARDIHAVRLHKGIPSRFALVPR---EG
                                                                                                                                                         IQLDQPTMMHDFAITENFVVVPDQQVVFKLPEMIRGGSPVVYDKNKVARFGILDKYAEDS
                                                                                                                                                                                                ENLGVASW-APLEG-VSAHPKVDEATGELMFFNY---SKAWPYMHYGVVGPDGKRKVYQG
                                                                                                                                                                                                                                                                            K-----RPGFG----AHGALKDSASTDIVVHNGEAIATF----YQCGEAYRLDPL-TL
                                                                                                                                                                                                                                                                                                                 RLMLFYARAAAGIVDPAHGT--GVANAGLVYFNGRLLAMSEDDLPYQ----VQITPNGDL
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RESULT 13
A70534
C;Species: Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: A70534
C;Accession: A70534
R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;
R; Colonor, R.; Davies, R.; Devilir, K.; Feltwell, T.; Gentles, S.; Hamilin, N.; Ho
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Rature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A; Reference number: A70500; MUID:98295987
A; Accession: A70534
A; Status: preliminar; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Residues: 1-501 <COL>
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 GE-EDEGYILCFVHDEKTWKSELQIVNAVSLEVEATVKLPSRVPYGFHGTF
                                                                                                                                          TPPDSIFNESDENLKSVLSEIRLNLKTGESTRRPIISNEDQQVNLEAGMVNRNMLGRKTK
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                                                                                                                                                                                                                   YYDKNKVARFGILDKYAEDSSNIKWIDAPDCFCFHLWNAWEEPETD-EVVVIG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148;
                                                  FAYTVGIEGGFLVGAGAALSTP-----LYKQDCVTGSSTVASLDPDLLIGEMVFVPNPS
                                                                                                                     FDRDRRGPGGDS--RPSLDRWTINLATGAVTAE---CRDDRA--QEFPRINETLVGGPHR
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27.9%;
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Pred. No. 2.3e-27;
6; Mismatches 195;
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hypothetical protein - Synechocystis C; Species: Synechocystis sp. C; Spariety: PCC 6803 C; Date: 25-Apr-1997 #sequence_revisio
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A;Cross-references: GB:Z95210; GB:AL123456; NID:g3261757; A;Experimental source: strain H37Rv C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987
A;Accession: A70582
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A; Residues: 1-502 <COL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; nucleic acid sequence not shown; translation
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                                                --LPSRVPYGFHGTFIGADDLAK
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LALPERISSGTHSAWVPGAELRR
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                                                                                                           HECYSFGDGVYGSETAMAPRVGSSAEDDGYLVTLTTDMNDDASYCLVFDAARPGDGPICK
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Pred. No. 1.7e-26;
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#sequence_revision 25-Apr-1997 #text_change 08-Oct-1999

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PCC 6803

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A;Reference number: S74322; MUID:97061201
A;Accession: S76169
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-490 <KAN>
A;Residues: 1-490 <KAN>
A;Cross-references: EMBL:D90914; GB:AB001339; NID:g1653477; PIDN:BAA18428.1; PID:d10191/A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: S76169
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
Search completed: July 19, Job time: 67 sec
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Matches 138; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 PKTADPSVQIAGNFAP-----VNEQPVRRNL---PVVGKLPDSIKGVYVRNGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 DRPLKHP-----FDGDGMVTAFKFPGDGRVHFQSKFVRTQGYVEEQKAGKMIYRGVFGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                            VNRNMLGRKTKFAYLALAE-----PWPKVSGFAKVDLTTGEVKKHLYGDNRYGGEPLFL 534
                                                                                                                                                                                                                                                               SICYNSLPQV--DTDGDFRSTNFD---NLDPGQLWRFTIDPAAATVEKQLMVSRCCEFPV
                                                                                                                                                                                                                                                                                                                                                                           -IRG-GSPVVYDKNKVARFGILDKYAEDSSNIKWIDAPDCFCFHLWNAWEEPETDEVVVI 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                      YLKYFRFSPDGTKSPDVEIQLDQPT------MMHDFAITENFVVVPDQQVVFK-LPEM- 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGEGG-EEDEGYILCFVHDEKTWKSELQIVNA--VSLEVEATVKLPSRVPYGFHGTF 588
                                                                                                                                                                                    VHPQQVGRPYRYVYMGAAHHSTGNAP----LQAILKVDLESGTETLRSFAPHGFAGEPIFV
                                                                                                                                                                                                                                                                                                   GSCMTPPDSIFNESDENLKSVLSEIRLNLKTGESTR---RPIISNEDQQVNL----EAGM
                                                                                                                                                                                                                                                                                                                                              GLRGAGECVQFHPDKPAQIILVPR---DGGEIKRIPVQAGFVFHHANAFE--ENGKIILD 318
                                                                                                                                                                                                                                                                                                                                                                                                                                 TUTLLELDPQGK-----LLRQKTETFPGFAFIHDFAITPHYAIFLQNNVTLNGLPYLF 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LHGHTGIARLMLFYARAAAGIVDPAHG-----TGVANAGLVYFNGRLLAMSEDDL 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPTSSPSQR----SYSPQDWLRGYQSQPQEWDYWVEDVEGSIPPDLQGTLYRNGPGLLEIG
                                                                                                    PRPGGVAEDDGWLLCLIYKADLHRSELVILDAQDITAPAIATLKLKHHIPYPLHGSW 487
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                   2002, 10:12:10
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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Match
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Gapop 10.0 , Gapext 0.5
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3150
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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MASFTATAAVSGRWLGGNHT.....VPYGFHGTFIGADDLAKQVV 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
    В
DNAA_PROMI
PAKI_SCHPO
PGCV_CHICK
CAD5_MOUSE
FAS_HUMAN
APCE_FREDI
SYFB_AQUAE
CYAA_USIMA
GLGS_BRANA
MASZ_MYCTU
YP72_CAEEL
CP74_ARATH
SLP1_YEAST
KDPG_SCHPO
UCR2_SCHPO
UCR2_SCHPO
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UCR2_SCHPO
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UCR2_SCHPO
ULTA_BRANA
TYCB_BRANA
TYCB_BRANA
TYCB_BRANA
AROC_WEIHE
F72_MYCMY
Y893_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105224
090953 gallus gall
p5528 mus musculu
p49327 homo sapien
p1656 fremyella d
067620 aquifex aeo
p49606 ustilago ma
09m462 brassica na
01433 schizosacch
p52417 vicia faba
p27742 emericella
031097 bacillus su
p52081 staphylococ
050596 mycobacteri
009221 caenorhabdi
096221 caenorhabdi
096221 caenorhabdi
096221 saccharomyc
014019 schizosacch
p78761 schizosacch
p39581 bacillus su
p32567 saccharomyc
030408 b tyrocidin
092269 penicillium
09jhya rattus norv
09jxz neisseria m
p29555 drospojila
p16310 rattus norv
p55118 pasteurella
p16310 rattus norv
p55118 pasteurella
p16310 mycoplasma
094467 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P25623 saccharomyc
P22837 proteus mir
P50527 schizosacch
Q90953 gallus gall
P55284 mus musculu
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Qy	Db	Qy	рb	Qy	Db .	οv	z w o	SQ	X X	ב ק	2 2	33	38	33	38	200	G 22	RP RA	R P.	RA RA	RP	N X	88	80	S E	DI	DT.	A ID	RES								
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YACRETQTNRFVQERQLGRPV	APALPPSRKQNF1	VGI	PKTVPISISQPPLQPQS	PKQSSNSPAIVVKPKAKESNTKQMNLFQRAAAAALDAAEGFLVSHE	QRRPTYSSSKSNNWTPGEASDTPPLPPHATPK-NVDAPVTADTP	YCSSLPMASRVTRKLNVSSAL-	; Length 870; 95; Indels 1	277 CRC64;				tp://www.isb-s	as its content	are no restr	thro		databases.		databases.	aeger I., Huse		•	la; Saccharomycetes Lromyces.	•	intergenic region						P42799 P44523 Q02907	P3314	P0800	P3853	P5511	Q6084 P3224	01397
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                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93:27-34(1990).

FUNCTION: PLAYS AN IMPORTANT ROLE IN THE INITIATION AND REGULATION OF CHROMOSOMAL REPLICATION. BINDS TO THE ORIGIN OF REPLICATION;

IT BINDS SPECIFICALLY DOUBLE-STRANDED DNA AT A 9 BP CONSENSUS

(DNAA BOX): 5'-TTATC(C/A)A(C/A)A-3'. DNAA BINDS TO ATP AND TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE DNAA FAMILY.
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                                                                                                                               PF00308; bac_dnaA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 otide sequence of a Proteus mirabilis DNA 60K-rnpA-rpmH-dnaA-dnaN-recF-gyrB region
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31 (Rel. 19, Last sequence upda
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Best Local Similarity
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              Wigler
"Shk1,
                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE-96112805; PubMed-8846783;
Ottilie S., Miller P.J., Johnson D.I., Creasy
Bagrodia S., Forsburg S.L., Chernoff J.;
"Fission yeast pakl+ encodes a protein kinase
Cdc42p and is involved in the control of cell
EMBO J. 14:5908-5919(1995).
                                                                                                                                                                                                                                                                                                                                   Serine/threonine-protein kinase pakl/shkl (EC PAK1 OR SHK1 OR ORB2 OR SPBC1604.14C.
                                               SEQUENCE OF 119-658 FROM N.A. MEDLINE=95320235; PubMed=7597
                                                                                 Beck A., Reinhardt R
Submitted (DEC-1998)
                                                                                                          STRAIN=972;
                                                                                                                     SEQUENCE FROM
                                                                                                                                                         SEQUENCE FROM Marcus S.;
                                                                                                                                                                                                                                                                                   Schizosaccharomyces.
NCBI_TaxID=4896;
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
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30-MAY-2000
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01-OCT-1996
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                                     Marcus
                                                                                                                                             Submitted (APR-1997)
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a homolog of the protein kinases,
                          . .
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                                      Polverino
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(Rel. 39, Last sequence up
(Rel. 39, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -RLNLKTGESTRRPIISN 469
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                                                                                                                                                                    N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                   PubMed=7597098;
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              Saccharomyces
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                                                                                M., Rajandream M.,
EMBL/GenBank/DDBJ
                                                                                                                                             EMBL/GenBank/DDBJ
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Pred. No. 0.
   component
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                                     Robbins
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               cerevisiae
   of a
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   Ras/Cdc42 signaling
                                                                                              .A.,
                                                                                                                                                                                                                                     C.L.,
                                                                                                                                             databases
                                                                                                                                                                                                   that interacts with polarity and mating
                                                                                   databases
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                                     Cobb M.H.,
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              Ste20
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               and mammalian
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Best Loc
Matches
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Pfam: Pro0069; pkinase; 1.
PRINTS; PRO0109; TYRKTN*C-
SMART; SMO0706
                                                                                                                                                                                                                                                                                                                                                   Phosphorylation.
DOMAIN 85
DOMAIN 234
DOMAIN 246
DOMAIN 263
DOMAIN 366
NP_BIND 392
BINDING 415
                                                                                                                                                                                                                                                                                                     NP_BIND
BINDING
ACT_SITE
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00285; PBD; 1.

SMART; SM00220; S_TKC; 1.

PROSITE; PS50108; GB; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1

PROSITE; PS50011; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000095;
InterPro; IPR002290;
InterPro; IPR001245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     module
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000719;
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 448
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                                                                                                                      118
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                                                                                                                                                                     83
                                                                                                                                                                                                                 18 NHTQPPLSSSQSSDL------SYCSSLPMASRVTRKLNVSSALHTPPALHFPKQSS
                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                   Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ule in the fission yeast Schizosaccharomyces pombe.";
c. Natl. Acad. Sci. U.S.A. 92:6180-6184(1995).
FUNCTION: FORMS AN ACTIVATED COMPLEX WITH GTP-BOUND CDC42. ACTS IN SIGNAL TRANSDUCTION. INVOLVED IN THE CELL POLARITY AND MATING. MAY INTERACT WITH BYR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTM: AUTOPHOSPHORYLATED ON SERINE RESIDUES. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STE20 SUBFAMILY.
DTFFYKSELWMVMEYMRGGSLTEVVTNNTL--SEGQIAAICKETLEGLQHLHENGIVHRD
                     --LFYARAAAGIVDPAHGTG----VANAGLVYFNGRLLAMSEDDLPYQVQITPNG----D
                                                                                                                                                                                           SHLQPTSATSSSSRLYPSRPAPTPPASSSSSPLLSSQTVKTTTSNASRQPSPLVSSKSTD 296
                                                                     HAVKFEHGSAS -- YACRFTQTNRFVQERQLGRPVFPK -- - AIGEL -- --
                                                                                             ATPQKVEAPSAPRLQKRAPRQ-----QSNDSAVLAKLQSICNPKNPTLLYRNF
                                                                                                                    DPSVQIAGNFAPVNEQPVRRNLPVVGKLPDSIKGVYVRNGANPLHEPVTGHHFFDGDGMV
                                                                                                                                             NIIRSHSPVLLTPQTLSTSETKHIRPNNSTPYQRRAETSTK---
                                                                                                                                                                  N-----SPAIVVKPKAKESNTKQM-----NLFQRAAAAALDAAEGFLVSHEKLHPLPKTA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L41552; AAB52609.1;
P00518; 1PHK.
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88; Conser
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237
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PAK_box_P21_Rho_
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                                                                                                                                                                                                                                                                                                       MW;
                                                                                                                                                                                                                                           61;
                                                                                                                                                                                                                                                                                                              PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
GLQH -> LYSD (IN REF. 1).
R -> P (IN REF. 1).
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                                                                                                                                                                                                                                                    Score 107.5;
Pred. No. 2.
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POLY-SER.
POLY-SER.
                                                                                                                                                                                                                                                                                                     -> P (IN REF. 1)
69D72E5C925021E5
                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as
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                                                                                                                                            -PKAV
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                      277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shinomura T., Nishida Y., Ito K., Kimata K.; "cDNA cloning of PG-M, a large chondroitin sulfate proteoglycan expressed during chondrogenesis in chick limb buds. Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35,
01-NOV-1997 (Rel. 35,
16-OCT-2001 (Rel. 40,
                                                                                                             EMBL; X60226; CAA42787.1;
EMBL; D13542; BAA02742.1;
HSSP; P20693; 1HLJ.
                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          spliced multiforms of PG-M and their relationships J. Biol. Chem. 268:14461-14469(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93300846; PubMed=8314802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archosauria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Versican core protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q90953; Q90945;
01-NOV-1997 (Re
                                                                                                                                                                                   entities requires a
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                                                                       [nterPro;
                                                                                  [nterPro;
                                                                                                   [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         355
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                                                                                                                                                                                                                                                                             (By similarity).

SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V SIMILARITY: CONTAINS 2 LINK DOMAINS.

SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                          ALTERNATIVE PRODUCTS: At least 2 isoform V1; are produced by alternative splicing TISSUE SPECIFICITY: Prechondrogenic cond
                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Secreted; extracellular ALTERNATIVE PRODUCTS: At least 2 isoforms; VO
                                                                                                                                                                                                                                                                                                                                                                                                                                                             JIOL. Chem. 268:14461-14469(1993).

FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part connecting cells with the extracellular matrix.
                                                                                                                                                                                                                          European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                 DEVELOPMENTAL STAGE: Disappears after
                                                                                                                                                                                                                                                                                                                                                                                 developing limb buds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    hyaluronic acid
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                                                                                                                                                                                                                                                       SWISS-PROT entry is
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                                                                                                                                                                    an email to license@isb-sib.ch).
IPR000742;
IPR001881;
IPR003599;
IPR003006;
IPR000538;
IPR000436;
                                                                                                                                                                                                                                          the
                                                                                    IPR000561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
e protein precursor (Large fibroblast
sulfate proteoglycan core protein 2)
                                                                                                                                                                                                                                       ROT entry is copyright. It is produced through a collaboration Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEGHORN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Eutel
Neognathae; Galliformes; Phasianidae;
                                                  Asx_hydroxyl.
EGF-like.
EGF_2.
EGF_Ca.
                                                                                                                                                                                   license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Limb bud;
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(PG-M).
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InterPro; InterPro;

[nterPro; [nterPro;

Ig.MHC. Link. Sushi_SCR_CCP

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PROSITE; PS01241; LINK; 2.

PROSITE; PS00615; C_TYPE_LECTIN_1; 1

PROSITE; PS50041; C_TYPE_LECTIN_2; 1

Glycoprotein; Proteoglycan; Lectin; Signal; Repeat; EGF-like Acmai-
CARBOHYD
CARBOHYD
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DISULFID
CARBOHYD
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SIGNAL
CHAIN
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SMART; SN
PROSITE;
PROSITE;
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SMART;
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SMART;
SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tam; PF00193; X1Ink; 2.
TroDom; PD000918; Link; 2.
ART; SM00032; CCP; 1.
ART; SM00034; CLECT; 1.
ART; SM00019; EGF_CA; 1.
RT; SM00001; EGF_11ke; 1.
RT; SM00409; IG; 1.
T; SM00445; LINK: 7.
TTE; PS00445; LINK: 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00008;
PF00047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS00010;
PS00022;
PS01186;
PS01187;
PS011241;
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 acid;
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EGF_1; 2.
EGF_2; 1.
EGF_CA; 2.
 lectin_c.
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              VERSICAN CORE I IG-LIKE V-TYPE LINK 1. EGF-LIKE 2. CAI C-TYPE LECTIN. SUSHILARITY. BY SIMILARITY. BY SIMILARITY
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               (GLCNAC
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V-TYPE DOMAIN
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 ISOFORM
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              (POTENTIAL)
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
            SEQUENCE FROM N.A.,
STRAIN-BALB/C; TISSU
MEDLINE=97364256; Pu.
Matsuyoshi N., Toda
Takeichi M., Imamura
                                                                                                                                                                                                                                                            LT 5

LMOUSE

CAD5_MOUSE

STANDARD;

PRT; 783 AA.

P55284; 035542;

01-CCT-1996 (Rel. 34, Created)

01-CCT-1996 (Rel. 34, Last sequence update)

16-CCT-2001 (Rel. 40, Last annotation update)

Vascular endothelial-cadherin precursor (VE-cadherin)

CDH5.
                                                    [2]
SEQUENCE
                                                                                      Breier G., Breviario F., Caveda L., Berthier R., Schnigotsch U., Vestweber D., Risau W., Dejana E.; "Molecular cloning and expression of murine vascular cadherin in early stage development of cardiovascular Blood 87:630-641(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1231
                                                                                                                                                       TISSUE=Brain capillary;
MEDLINE=96141083; PubMed=8555485;
                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1496
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                                                                                                                                                                                                                                                                                                                                                                                                         LLITNESSGDGS--TESDLS-RSVFTEI-LTMSSHEDSEK 1656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MASFTATA-AVSGRWLGGNHTQPPLSSSQSSDLSYCSSLPMASRVTRKLNVSSALHT---
                                                                                                                                                                                                                                                                                                                                                                                                                                 VVIGSCMTPPDSIFNESDENLKSVLSEIRLNLKTGESTRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVYDKNKVARFGILDKYAEDSS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----EASGTMQPSKAGEVMGAFEVTQPTA--DVAMLE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YFRFSPDGTKSPDV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEDDLPYQVQITPNGDLKTVGRFDFDGQLESTMIAHPKVDPESGELFALSYDVVSKPYLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --LGRPVFPKAIGELHGHTGIARLMLFYARAAAGIVDPAHGTGVAN-AGLVYFNGRLLAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TDIRLYVIQITGNDTDHPVNEFLDLFSRHILPHAVDETHTDAESAQTEPCTSDSVQDSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --IKGVYVRNGANPLHEPVTGH-HFFDGDGMVHAVKFEHGSASYACRFTQTNRFVQERQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VEPE----IDKEYFTSSTATAVARPTAPPTVMEATEALQPQEVSPTSH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSHEKLHPLPK------TADPSVQIAGN-FAPVNEQPVRRNLPVVGKLPDS- 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAVDKIQPTSASKPFVSSKSPRII--PEEDEEVTSSDIIVIDESISPSKASAEDDLTGKM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----QQVTSAPKSTKAEEARSD---QIES--VAHSK-NVTFSQINETNTFIISET---
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M., Imamura S.; evidence of the
                                                                                                                                                                                     FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -PPALHFPKQSSNSPATVVKPKAKESNTKQMNL-----FQRAAAAALDAAEGFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                   N.A.
                        56; PubMed=9220534;
Toda K.-I., Horigu
                                                   TISSUE-Breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                               AND FUNCTION
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 critical role
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                         Horiguchi Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61;
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Pred.
                                                   carcinoma;
                                                                                                                                                                                                                       Craniata; Vertebrata; Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -NIKWIDAPDCFCFHLWNAWEE---PETDEV
 of cadherin-5
                         Tanaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                   vascular endothelial-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191;
                                                                                                                                                                                                                         Muridae;
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                         Nakagawa
in murine
                                                                                                                                                                                                                         Murinae;
                                                                                                     system.";
                                                                                                                                                                                                                                                                         (Cadherin-5).
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Best Local Sin
Matches 128;
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CARBOHYD
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal.
SIGNAL
PROPEP
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VASCULAR INTEGRITY.";
PROC. ASSOC. AM. Physicians 109:362-371(1997).
-I- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.
-I- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.
-I- FUNCTION: CADHERINS ARE THE SENTENCE IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE SORTING OF HETEROGENEOUS CELL TYPES. THIS CADHERIN MAY PLAY A IMPORTANT ROLE IN ENDOTHELIAL CELL BIOLOGY THROUGH CONTROL OF THE INTERCELLULAR JUNCTIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00232; CADHERIN_1; 3. PROSITE; PS50268; CADHERIN_2; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00028; cadherin; 5.
Pfam; PF01049; Cadherin_C_term;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002126; Cadherin_C_term.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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                                                                                                                                                         112
                                                                                                                                                                                                113
217
                                      204
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                                                                                                                                                                                                                                   MHIDEEKNESLPHYVKDQSNVNRQNAKYVLQGEFAGKIFGVDANTGNVLAYERLDREKVS
                                                                                                                                                                                                                                                                        LHFPKQSSNSPAIVVKPKAKESNTKQMNLFQRAAAA----ALDAAEGFLVSHEKLHP----
QAEYKIVVETQDALG-LRGESGTATVMI---
                                      QLGRPVFPK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X83930; CAA58782.1; -. D63942; BAA22617.1; -. P15116; INCJ. MGI:105057; Cdh5.
                                                                             AVDADDPTVAGHATVLYQIVKGNEYFSIDNSGLI--
                                                                                                                                                       EYFLTALIVDKNTNKNLEQPSSFTVKVHDINDNWPVFSHQVFNASVPEMSAIGTSVIRVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; PR00205; CA;
SM00112; CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and this statement is not removed. requires a license agreement (See
                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                -LPKTADPSVQ
                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
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87847
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                                    AIGELHGHTGIARLMLFYARAAAGIVDPAHGTGVANAGLVYFNGRLLA
                                                                                                                                                                                                                                                                                                                               3.3%;
                                                                                                              LHEPVTGHHFF -- DGDGMVHAVKFEHGSASYACRFTQTNRFVQER
                                                                                                                                                                                                                                                                                                                 101;
                                                                                                                                                                                                                                                                                                                                                                                                                 ¥.
                                                                                                                                                                                                                                                                                                             Score 105; DB Pred. No. 4.7; 01; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
CYTOPLASMIC
CADHERIN 1.
CADHERIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                  CADHERIN 3
CADHERIN 5
CADHERIN 5
SER-RICH.
N-LINKED (
N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane;
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240AF2D663BCE71C (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
VASCULAR ENDOTHELIAL-CADHERIN
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                            IAGNFAPVNEQPVRRNLPVVGKLPDSIKGVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GLCNAC...)
(GLCNAC...)
(GLCNAC...)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
                                                                                                                                                                                                                                                                                                                 242;
                                                                                                                                                                                                                                                                                                                                                    1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Usage
                                                                                                                                                                                                                                                                                                                                                    Length 783;
                                                                                                                                                                                                                                                                                                                                                                                                                 CRC64;
                                                                                                                                                                                                                                                                                                                 Indels 254;
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) (POTENTIAL).
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01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fatty acid synthase (EC 2.3.1.85) [Includes: JEC 2.3.1.41; EC 1.1.1.100; EC 4.2.1.61; EC 1.
                                                                                                                                                                                                                  (2)
SEQUENCE OF 753-758 AND 1285-1297.
MEDLINE-94294385; PubMed-8022791;
Kuhaida F.P., Jenner K., Wood F.D.,
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                  "Fatty acid Synthesis: a potential selective target for antineoplastic therapy."; proc. Natl. Acad. Sci. U.S.A. 91:6379-6383(1994).
-I-FUNCTION: FATTY ACID SYNTHETASE CATALYZES THE FORMATION LONG-CHAIN FATTY ACIDS FROM ACETYL-COA, MALONYL-COA AND THIS MULTIFUNCTIONAL PROTEIN HAS 7 CATALYTIC ACTIVITIES ACYL CARRIER PROTEIN.
                                                                                                                                                                                             MEDLINE=94294385; PubMed=80
Kuhajda F.P., Jenner K., Wo
Dick J.D., Pasternack G.R.;
                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci.
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Mammalia; Eutheria;
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Jayakumar A., Tai M.-H., Huang W.-Y.,
Abu-Elheiga L., Chirala S.S., Wakil S.
"Human fatty acid synthase: properties
Proc. Natl. Acad. Sci. U.S.A. 92:8695-
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Brain;
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Primates;
Acetyl-CoA
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+ N malonyl-CoA +
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pfam; pF00109; ketcacyl-synt; 1.
pfam; pF002801; ketcacyl-synt_C; 1.
pfam; pF00550; pp-binding; 1.
pfam; pF00975; Thioesterase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +

NADP(+) = 3-oxoacyl-(acyl-carrier protein] + NADPH.

CATALYTIC ACTIVITY: (3R)-3-hydroxypalmitoyl-(acyl-carrier protein]
= 2-hexadecenoyl-(acyl-carrier protein) + H(2)0.

CATALYTIC ACTIVITY: Acyl-(acyl-carrier protein) + NADP(+) = trans-
2,3-dehydroacyl-(acyl-carrier protein) + NADPH.

2,3-dehydroacyl-(acyl-carrier protein) + NADPH.
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CATALYTIC ACTIVITY: Malonyl-CoA + [acyl-carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     long-chain fatty acid + (N+1) CoA + N CO(2) + 2N NADP(+).
CATALYTIC ACTIVITY: Acetyl CoA + [acyl-carrier protein] = CoA +
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SUBUNIT: HOMODIMER, WHICH IS ARRANGED IN
TISSUE SPECIFICITY: PROMINENT EXPRESSION
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THIOESTERASE (BY SIMILARITY).
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MALONYLTRANSFERASE (BY SIMILARITY).
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P16566;
01-AUG-1990 (Rel. 15, Created)
01-BUG-1990 (Rel. 15, Last sequence update
01-DEC-1992 (Rel. 24, Last annotation update
Phycobilisome 120 kDa linker polypeptide,
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                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long
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              HSSP; P00318;
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Bacteria; Cyanobacteria; Nostocales; Rivula
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                                                                                                                                                                                                             SIMILARITY: THE REPEATED DOMAINS ARE SIMILAR TO THE N-TERMINAL REGIONS OF PHYCOCYANIN ROD LINKER POLYPEPTIDES.
SIMILARITY: THE PHYCOBILIN-LIKE DOMAINS ARE SIMILAR TO PHYCOBI
                                                                                                                                                                                                                                                          POLYPEPTIDE, AND THE ANCHOR POLYPEPTIDE LCM.
SUBCELLULAR LOCATION: ANCHORS THE PHYCOBILISOME
TO THE STROMAL SURFACE OF THE THYLAKOID MEMBRANE
                                                                                                                                                                                                                                                                                                     SUBUNIT: PHYCOBILISOMES OF THIS ORGANISM ARE COMPOSED OF A CYLINDER CORE, FROM WHICH SIX RODS RADIATE. THE CORE IS AND COMPOSED OF ALLOPHYCOCYANIN ALPHA AND BETA CHAINS, AND OF T MINOR COMPONENTS: THE ALLOPHYCOCYANIN ALPHA-B CHAIN, A 18.3
                                                                                                                                                                                                                                                                                                                                                                  2. Natl. Acad. Sci. U.S.A. 87:2152-2156(1990).
EUNCTION: THIS PROTEIN IS POSTULATED TO ACT BOTH AS TERMINAL ENERGY ACCEPTOR (BY ITS PHYCOBILIN-LIKE DOMAINS) AND AS A LII POLYPEPTIDE (BY ITS REPEATS AND ARMS) THAT STABILIZES THE PHYCOBILISOME CORE ARCHITECTURE.
                                                                                                                                                                                                 FROM VARIOUS SPECIES
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                                                                        and this statement is not removed. requires a license agreement (See an email to license@isb-sib.ch).
              1B33
                                           AAA24873.1;
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Matches 71
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R Pfam; PF00427; PBS_linker_poly; 4.

R Pfam; PF00502; Phycobilisome; 2.

Phycobilisome; Electron transcriptions
                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Phenylalanyl-trNA synthetase beta chain (EC 6.
tRNA ligase beta chain) (PheRS).
PHET OR AQ_1730.
Aquifex aani
                                 MEDLINE-98196666; PubMed-9537320;
Deckert G., Warren P.V., Gaasterland T., Young
Deckert B., Overbeek R., Snead M.A., Keller M
Feldman R.A., Short J.M., Olson G.J., Swanson
"The complete genome of the hyperthermophilic
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Nature 392:353-358(1998).
-!- CATALYTIC ACTIVITY: ATP + L-phenylalanine
diphosphate + L-phenylalanyl-tRNA(Phe).
                              aeolicus
                                                                                      STRAIN-VF5
                                                                                               SEQUENCE FROM N.A.
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Bacteria; Aquificales;
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Pred. No. 8.1;
47; Mismatches
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Last sequence update)
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between
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Aminoacyl-tRNA synthetase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (Some send an email to license@isb-sib.ch).
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SIMILARITY).
SUBCELLULAR LOCATION: C
SIMILARITY: BELONGS TO
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                                                                                                                                                                     GMVNRNMLGRKTKFA-YLALAEPWPKVSGFAKVDLTTGEVKKHLYGDNRYGGEPLFLP---
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775 AA;
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license agreement (See http://www.isb-sib.ch/announce/
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20.7%;
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O THE PHENYLALANYL-TRNA
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                                                                                                     VKEILDALEIPNEI-MRCGVEVLVPS-----
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Pfam; PF00211; guanylate_cyc; 1.
Pfam; PF00560; LRR; 18.
Pfam; PF00481; PP2C; 1.
SMART; SM00044; CYCC; 1.
SMART; SM00370; LRR; 6.
SMART; SM00370; LRR; 7YP; 2.
SMART; SM00332; PP2CC; 1.
SMART; SM00314; RA; 1.
SMART; SM00314; RA; 1.
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                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ustilaginomycetidae;
NCBI_TaxID=5270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ustilago maydis (
Eukaryota; Fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genes
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                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gold S., Duncan G., Barrett K., Krons
"cAMP regulates morphogenesis in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UAC1 OR REM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adenylate
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                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                            interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diphosphate.
SIMILARITY: BELONGS TO ADENYLYL CYCLARE CLASS-3 FAMILY.
SIMILARITY: CONTAINS 21 LEUCINE-RICH REPEATS (LRR).
SIMILARITY: CONTAINS A PP2C-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METABOLISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION:
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IPR00151; LRR.
IPR003592; LRR_cut.
IPR003591; LRR_typ.
IPR001932; PP2C_domain.
                                                                                                                                                                                                                                                                                            IPR000159; RA.
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M BY CATALYSING T
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Basidiomycota; Ust
ae; Ustilaginales;
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LRR 21.
PP2C-LIKE.
CATALYTIC.
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                                                                                                                                                                                                          CAMP
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fungal pathogen Ustilago
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Best Local
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01-MAR-2002 (Rel. 41, Last sequence update)
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Created)
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01-MAR-2002
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                                                                                                                                                                                                                                                                             "Isolation and analysis of a cDNA clone encoding ADP-glucose pyrophosphorylase in the plastids of Oilseed rape (Brassica napus).";
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-CV. Drakkar; TI
Zawodny S., Martini N.
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Eukaryota; Viridiplantae;
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                    PATHWAY: STARCH BIOSYNTHESIS.
SUBUNIT: HETEROTEFRAMER.
SUBCELLULAR LOCATION: Chloroplast
TISSUE SPECIFICITY: LEAVES.
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BELONGS
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PROSITE; PS00809; ADP_GLC_PYROPHOSPH_2; 1.
PROSITE; PS00810; ADP_GLC_PYROPHOSPH_3; 1.
Glycogen biosynthesis; Transferase; Nucleotidyltransferase;
                                                                                                                                                     Wood V., Rajandream M.A.,
Submitted (AUG-1997) to t
                                                                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast) Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales; Schizosaccharomy
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TRANSIT
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InterPro; IPR001825; NTP_transferase.
Pfam; PF00483; NTP_transferase; 1.
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                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              SCR1 OR SPBC1D7.02C.
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an email to license@isb-sib.ch).
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27.0%;
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                                                                                                                                                                                                                                        Schizosaccharomycetaceae;
                                                                                                                                                    Barrell B.G., Skelton J., Churcher C.M.; ne EMBL/GenBank/DDBJ databases.
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Pred. No. 4.7;
27; Mismatches
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GLGT_VICFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last sequence update)
01-MRR-2002 (Rel. 41, Last annotation update)
Glucose-1-phosphate adenylyltransferase small subunit 2, chloropla
precursor (EC 2.7.7.27) (ADP-glucose synthase) (ADP-glucose
precursor (EC 2.7.7.27) (ADP-glucose synthase) (ADP-glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
Vicia faba (Broad bean).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Vicia.
                                                                                                                                                                                GLGT_VICFA P52417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMARR; SM00355; ZnF_C2H2; 2.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
PROSITE; PS50157; ZINC_FINER_C2H2_2; 2.
DNA_binding; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000822; Znf-C2H2. Pfam; PF00096; zf-C2H2; 2. PRINTS; PR00048; ZINCFINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z98270; CAB10978.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                             AGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
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                                                                                                                                                                                                                                                                         AHFRYQRRSRPVSPCS-TAPSSPTFSTRSFSP----TPDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATAAVSMSY--PHHYSASVQQQQATFVSNGQPHNLPAQAQPATIYGIPDALHTTQNGTTI 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATAAVSGRWLGGNHTQPPLSSSQSSDLS--YCSSLPMASRVTRKLNVSSALHTP---PAL
                                                                                                                                                                                                                                                                                                      AHPKVDPESGELFALSYDVVSKPYLKYFRFSPDGTKSPDV 335
                                                                                                                                                                                                                                                                                                                                                                GIVDPAHGTGVANAGLVYFNGRLLAMSEDDLPYQVQITPNGDLKTVGRFDFDGQLESTMI 295
                                                                                                                                                                                                                                                                                                                                                                                               FTKYTNGS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HVTGTPPGAVSQRSEPDSRLSSMNEMQLLASAAANQLDAA-----PRIT-PT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HFPKQSSNSPAIVVKPKAKESNTKQMNLFQRAAAAALDAAEGFLVSHEKLHPLPKTADPS 120
                                                                                                                                                                                                                                                                                                                                                                                                                          AVKFEHGSASYACRFTQTNRFVQERQLGRPVFP---KAIGELHGHTGIARLMLFYARAAA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VQIAGNFAPVNEQP-VRRNLPVVGKLPDSIKGVYVRNGANPLH-EPVTGHHFFDGDGMVH 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                           KSSGVNLMPLSNAPSPPKQMNVVGSLPSS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                r protein; Zinc;
G 26 48
G 54 78
G 81 97
509 548
164 167
375 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                    -TAYAPQSLRYAH-----YNYLPYSRPSVSNG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48
78
97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.2%;
21.8%;
                                                                                                                                                                                                                                                                                                                                                                                               SNSLYSNSSMQTPYLPSKSNSSTSLHSMYGVGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Metal-binding; Rec2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 101.5; 1
Pred. No. 5.3;
8; Mismatches
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SER-RICH.
POLY-GLN.
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                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FE6CCCF7E54A8CDB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repressor; Zinc-finger;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNTSPNHLASVPNRGLTSNSSTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                    FDDDSSSSDF
                                                                                                                       chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81;
                 Rosidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                               344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsendanemail to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Planta 195:352-361(1995).

- IF UNCTION: THIS PROTEIN PLAYS A ROLE IN SYNTHESIS OF STARCH.
- IT CATALYSES THE SYNTHESIS OF THE ACTIVATED GLYCOSYL DONOR,
- ADP-GLUCOSE FROM GLC-1-P AND ATP.
- I- CATALYTIC ACTIVITY: ATP + alpha-D-glucose 1-phosphate =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00808; PROSITE; PS00809;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X76941; CAA55260.1; -.
InterPro; IPR001825; NTP_transferase.
Pfam; PF00483; NTP_transferase; 1.
PROSITE; PS00808; ADP_GLC_PYROPHOSPH_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Weber H., Heim U., Borisjuk L., Wobus U.;
"Cell-type specific, coordinate expression
pyrophosphorylase genes in relation to star
seed development of Vicia faba L.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95218601; PubMed=7766042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
         216
                                                                  168
                                                                                                                                                                                 117
                                                                                                                                                                                                                                          132
                                                                                                                        182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ROSITE; PS00809; ADP_GLC_PYROPHOSPH_2; 1.
ROSITE; PS00810; ADP_GLC_PYROPHOSPH_3; 1.
Llycogen biosynthesis; Transferase; Nucleotidyltransferase; Nullengene family; Starch biosynthesis; Allosteric enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                 62
                                                                                                                                                                                                                                                                                                                                                          77
                                                                                                                                                                                                                                                                                                                                                                                                                10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Chloroplast (By similarity).

TISSUE SPECIFICITY: LEAVES AND SEEDS.

DEVELOPMENTAL STAGE: IT IS PRESENT IN YOUNG COTYLEDONS AT 14 DAYS AFFER FERTILIZATION (DAF) WHEN CELLS ARE STILL RAPIDLY DIVIDING.

AFFER FERTILIZATION (DAF) WHEN CELLS ARE STILL RAPIDLY DIVIDING.

LEVELS STEADILY ACCUMULATE UNTIL THE END OF THE CELL EXPANSION PHASE (35-40 DAF) AND WITH THE BECINNING OF THE SEEDS DESICCATION PHASE (35-40 DAF) AND WITH THE BECINNING OF THE SEEDS DESICCATION PHASE AT 50 DAF, THE LEVELS DECREASE TO VERY LOW LEVELS.

SIMILARITY: BELONGS TO THE BACTERIAL AND PLANTS GLUCOSE-1-
PHOSPHATE ADENYLYLTERANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diphosphate + ADP-glucose.
ENZYME REGULATION: ACTIVATED BY 3'PHOSPHOGLYCERATE,
BY ORTHOPHOSPHATE. ALLOSTERIC REGULATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PATHWAY: STARCH BIOSYNTHESIS. SUBUNIT: HETEROTETRAMER.
ELHGHTGIARLMLFYARAAAGIVDPAHGTGVANAGLVYFN--GRLLAMSEDDLPYQVQIT
                                                                                                                                                                           -----DIPVSNCLNSNISKIYVLTQFN---SASLNRHLSRAYASNLGGYKNEGFVEVLA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPLSSSQSSDLSYCSSLPMASRVTRKLNVSSALHTPPALHF-----PKQSSNSPAIVVKP 76
                                                         AQQSPENPNWFQGTADAVRQYLWLFEEHNVLEYLVLAGDHLYRMDYER-----FIQAHR
                                                                                                                                                                                                                                    EQPVRRNLPVVGKLPDSIKGYYVRNGANPLHEPVTGHHF-----FDGDGMVHAVK 181
                                                                                                                                                                                                                                                                                           KAVSDSKNSQTCLDPDASRSVL----GIILGGGAGTRLYPLTKKRAKPAVPLGANYRLI- 116
                                                                                                                                                                                                                                                                                                                                                 KA-KESNTKOMNLFORAAAAALDAAEGFLV---SHEKLHPL-PKTADPSVOIAGNFAPVN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               al Similarity 21.0
118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              family; Starch biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                     -HGSA----SYACRFTQTN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Cotyledon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 101;
Pred. No. 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHLOROPLAST (POTENTIAL).
GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             060647F683526EDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sion of
starch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Usage by and for commercial http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                two ADP-glucose
biosynthesis du
                                                                                                                  RFVQERQLGRPVFPKAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              restrictions
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RESULT 13
ACVS_EMENI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                          J. Biol.
                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                       "Delta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine synthetase from Aspergillus nidulans. Molecular characterization of the acva gene encoding the first enzyme of the penicillin biosynthetic pathway.

J. Biol. Chem. 266:12646-12654(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maccabe A.P., van Liempt H., Pallissa H., Unkles S.E., Pfeifer E., von Doehren H., Kinghorn J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Eurotiales; Trichocomaceae; Emericella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-Aug-1992 (Rel. 23, Created)
01-Aug-1992 (Rel. 23, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Delta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1992 (Rel.
01-AUG-1992 (Rel.
16-OCT-2001 (Rel.
                HSSP; P14687;
                           EMBL; X54853; CAA386
PIR; A40889; A40889.
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                                                                                                                                                                                                                                                                                                            INTERMEDIATES.
COFACTOR: CONTAINS
                                                                                                                                                                                                                                                                                                                                   3101. Chem. 266:12646-12654(1991).
FUNCTION: EACH OF THE CONSTITUENT AMINO ACIDS OF THE TRIPEPTIDE ACV ARE ACTIVATED AS AMINOACYL-ADENYLATES WITH PEPTIDE BONDS FORMED THROUGH THE PARTICIPATION OF AMINO ACID THIOLESTER
                                                                                                                                                                                                     SIMILARITY: CONTAINS 3 ACYL CARRIER DOMAINS
                                                                                                                                                                                                                                  SIMILARITY:
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                                                                          s requires a license agreement (See http://www.isb-sib.ch/announce,
an email to license@isb-sib.ch).
                                                                                        non-profit institutions as long as its content
and this statement is not removed. Usage by ar
requires a license agreement (See http://www.isb
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InterPro;

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30-MAY-2000 (Rel. :

30-MAY-2000 (Rel. :
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InterPro; IPR000379; Est_lip_thioest_actsite.
InterPro; IPR0003880; Phosphopant_attach.
InterPro; IPR001031; Thioesterase.
Pfam; PP00501; AMP-binding; 3.
Pfam; PF00501; AMP-binding; 3.
Pfam; PF00668; Condensation; 3.
Pfam; PF00505, pp-binding; 3.
Pfam; PF00950; Thioesterase; 1.
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BINDING
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PROSITE; PS00455;
PROSITE; PS50075;
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                                                                                                                                                                                                 GELFALSYDVVSKPYLKYFRFSPDGTKSPDVEIQLDQPTMMHDFAITENFV-----VVP
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39, Last sequence update,
39, Last sequence update)
sor (EC 3.13.8) (Phytate 3-phosphatase)
ssphate 3-phosphohydroiase).
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Pred. No. 1.1e+02
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DOMAIN 3 (VALINE-ACTIVATING).
ACYL CARRIER (ACP) 1.
ACYL CARRIER (ACP) 2.
ACYL CARRIER (ACP) 3.
ACYL CARRIER (ACP) 3.
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PHOSPHOPANTETHEINE (BY SIMILARITY).
PHOSPHOPANTETHEINE (BY SIMILARITY).
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"Isolation, characterization, molecular gene cloning, and sequencing
of a novel phytase from Bacillus subtilis.";

Appl. Environ. Microbiol. 64:2079-2085(1998).

-i- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
FROM PHYTATE. ONLY PHYTATE, ADP, AND ATP WERE HYDROLYZED (100, 75,
AND 50% OF THE RELATIVE ACTIVITY, RESPECTIVELY). HAS MAXIMAL
ACTIVITY AT PH 7 AND 55 DEGREES CELSIUS.

-i- CATALYTIC ACTIVITY: Myo-inositol hexakisphosphate.

-i- CATALYTIC ACTIVITY: Myo-inositol hexakisphosphate.

-i- COPACTOR: ISOLATED ENZYME REQUIRED CALCIUM FOR ITS ACTIVITY AND/OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Clostridium
Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWI
between
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STRAIN-VTT E-68013;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Pfam; PF02333; Phytase;
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VVPDQQVVFKLPEMIRGGSPVVYD----KNK-VARFGILDKYAEDSSNIKWIDAPDCFCFH
                                         YGRLYIAEEDEA----IWKFSAEPDGGSNGTVIDRADGRHLTRDIEGLTIYYAADGKGYL
                                                                            SGELFALSYDVVSKPYLKYFRFSPDGTKSPDVEIQLDQPTMMHDF-----
                                                                                                                                                      GLVYFNGRLLAM---SEDDL-PYQVQITPNGDL--KTVGRFDFDGQLESTMIAHPKVDPE
                                                                                                                                                                                                                                        RFTQTNRFVQERQLGRPVFP---KAIGELHGHTGIARLMLFYARAAAGIVDPAHGTGVANA
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383 AA;
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p52081;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Bifunctional autolysin precursor [Includes: N-acetylmuramoy1-L-alanine amidase (EC 3.5.1.28); Mannosy1-glycoprotein endo-beta-N-acetylglucosamidase (EC 3.2.1.96)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alanine amidase domain and an endo-beta-N-acetylglucosaminidase domain: cloning, sequence analysis, and characterization."; Proc. Natl. Acad. Sci. U.S.A. 92:285-289(1995).
  DOMAIN
                                                                                                              Cell wall;
                                                                                                                                                                                           Pfam;
                                                                                                                                                                                                                 InterPro; IPR002502; Amidase_2.
InterPro; IPR002901; Amidase_4.
                                                                                                                                                                                                                                                                             EMBL; D17366; BAA04185.1; -. EMBL; L41499; AAA99982.1; -.
                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (APR-1995)
-!- FUNCTION: ENDOHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-NCTC 8325-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus/Staphylococcus group;
NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillus/Clostridium gruBacillus/Staphylococcus group; Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus.
                                                                                     SIGNAL
                                                                                                                                          SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oshida T., Sugai M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95116542; PubMed=7816834;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glycopeptides.
SUBCELLULAR LOCATION: Secreted.
SUBCELLULAR LOCATION: Secreted.
PTM: UNDERGOES PROTEOLYTIC PROCESSING TO GENERATE THE EXTRACELLULAR LYTIC ENZYMES.
SIMILARITY: IN THE N. TERMINAL SECTION; BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mitted (APR-1995) to the EMBL/GenBank/DDBJ databases. FUNCTION: ENDORYDROLYSIS OF THE DI-N-ACCETYLCHITOSICSYL UNIT IN HIGH-MANNOSE CLYCOPEDFIDES AND ELYCOPROTEINS COMPAINING THE HIGH-MANNOSE CLYCOPEDFIDES AND STRUCTURE. ONE N-ACETYL-D-GLUCOSAMINE [(MAN)5(GLCNAC)2]-ASN STRUCTURE. ONE N-ACETYL-D-GLUCOSAMINE RESTOUE REMAINS ATTACHED TO THE PROTEIN; THE REST OF THE OLIGOSACCHARIDE IS RELEASED INTACT.

CATALYTIC ACTIVITY: Hydrolyses the link between N-acetylmuramoyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO FAMILY 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   residues and L-amino acid residues in certain bacterial cell-wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACETYLMURAMOYL-L-ALANINE AMIDASE FAMILY
                                                                                                                                                              ; PF01510;
; PF01832;
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4; 1.
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POTENTIAL.
BIFUNCTIONAL AUTOLYSIN.
N-ACETYLMERAMOYL-L-ALANINE AMIDA
ENDO-BETA-N-ACETYLGLUCOSAMIDASE.
                                                                                                           Multifunctional enzyme;
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1 MASFTATAAVSGRW
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Copyright (c) 1993 - 2000 Compugen
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/FCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/packfiles1.pep:*
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US-09-385-259-2
US-08-488-305A-6
US-08-928-361B-6
US-08-928-361B-6
US-08-928-361B-11
US-08-928-361B-5
US-08-928-361B-11
US-09-461-697-77
US-08-611-107-31
US-09-001-984C-106
US-08-097-829-4
US-09-568-102-3
US-09-568-102-3
US-09-568-486-3
US-09-625-188-18
US-08-725-587-188
US-09-625-188-18
US-09-625-188-18
US-08-725-459B-22
US-08-398-627-10
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Sequence 3, Appli
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Sequence 77, Appli
Sequence 31, Appli
Sequence 4, Appli
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Sequence 18, Appli
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KSEVVVQFPC	LKTVGRFDFDGQL	AVKE KEDE ARAP	11a Co -AG 	2.59-2 2. Application US/0 3. 2. Application US/0 40. 6201114 INFORMATION: INFORMATION INFO	222222222222222222
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LWGANYM 2	YLKYFRFS 3 : : PLQADKED 2 S 3	ELHGHT 2 : : : : : : : : : : : : : : : : : : :	533; ls 140; Gap HEPVTGHH 1 :: EVGSEPFYH 5	STATIONARY NIGHT BLI	Sequence 10, Sequence 20, Sequence 21, Sequence 21, Sequence 18, Sequence 18, Sequence 18, Sequence 2, Sequence 2, Sequence 5, Sequence 17, Sequence 16, Sequence 16, Sequence 12, Sequence 2, Sequence 4, Sequence 4, Sequence 6,
76	26 18 74	21 15 76 58	s 25; 69	BLINDNESS	Appl Appl Appl Appl Appl Appl Appl Appl

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                                                                                                                                            Best Local Similarity Matches 119; Conserv
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 5679772
                                                                                                                                                                                                                                                                                  TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 533 amino acids
                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Kohli, Vineet
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                     161
                                                                                                       105 VSHEKLHPLPKTADPSVQIAGNFAPVNEQPVRRNLP----VVGKLPDSIKGVYVRNGANP 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 7-JUNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-1
SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                     TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette, 3.5 inch, 1.44 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                   LH---EPVTGHHFFDGDGMVHAVKFEHGSASYACRFTQTNRFVQE------RQLGRPV 209
FEVGSEPF--YHLFDGQALLHKFDFKEGHVTYHRRFIRTDAYVRAMTEKRIVITEFGTCA 107
                                                                        MSSQVEHP---
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: 805 Third Avenue
New York City
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                                                                                                                                            Conservative
                                                                                                                                                                                                                                                      linear
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                                                                      ----AGGYKKLFETVEELSSPLTAHVTGRIPLWLTGSLLRCGPGL 49
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                                                                                                                                                           Score 209; DB 1;
Pred. No. 6.1e-13;
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                                                                                                                                            Mismatches
                                                                                                                                            222;
                                                                                                                                                                            Length 533;
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                                                                                                                                         Gaps
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RESULT 3
US-08-928-361B-30
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                                  NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
TELEFAX: 650-324-1678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF JUNE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: P
SOFTWARE: PatentIn
                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Carolyn Polypeptides, Glycoproteins, Peptides, Polypeptides, Glycoproteins, THEER FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM SPECIES INFECTIONS
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US-08-700-651-5
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                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application Patent No. 6015882
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Best Local
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum TITLE OF INVENTION: INFECTIONS FILE REFERENCE: 480.19-4(HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER FILING DATE: 1995-04-03
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                                                                                                                                                                                                                                                          APPLICANT: PETERSEN, CAROLYN APPLICANT: LEECH, JAMES APPLICANT: NELSON, RICHARD, C. APPLICANT: GUT, JIRI
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STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLGPSEQTQFSPEIEDGGIIPPEVAAANADKFKLSIPPSVPESIPEKDQKIDSISELMYD
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SOFTWARE: PatentIn Ver.
SEO ID NO 5
LENGTH: 1721
TYPE: PRT
                                                                                                                                                      Sequence 6, Application Patent No. 6071518 GENERAL INFORMATION:
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Best Local Similarity
Matches 125; Conserv
                                                                        APPLICANT: Petersen, (
TITLE OF INVENTION: PITITLE OF INVENTION: FITITLE OF INVENTION: FITITLE OF INVENTION: SI
                             CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY,
                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                     AGMVNRNMLGRKTKFAYLALAEPWPKVSGFAKV---DLTTGEVKKHLYGDNRYGGEPLFL 534
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                                                                                                                                                                                                                                                                                                     PGEGGEE 541
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PEPPIDES, POLYPEPPIDES, GLYCOPROTEINS,
THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
SPECIES INFECTIONS
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e, Suite 6
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Best Local S
Matches 125
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TOPOLOGY: linear
MOLECULE TYPE: protein
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PAPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 12-SEP-19
                                                                                                      1181 -IPGSLPGSLNYPSFNTPQQTDE-----ITGKPVDTVTGLPY--
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MEDIUM TYPE: Floppy disk
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mes 125; Conservative
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 AGMVNRNMLGRKTKFAYLALAEPWPKVSGFAKV---DLTTGEVKKHLYGDNRYGGEPLFL
                                                                                                                                      KLPEMIRG-----GSPVVYDKNKVARFGILDKYAEDSSNIKWIDAPDCFCFHLWNAWE 417
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20.6%; Pred. No. 0.0044;
rative 85; Mismatches 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.7
Best Local Similarity 19.9
Matches 113; Conservative
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ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/026,062 FILING DATE: 13-SEP-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                   PTTGL-----PFNPP-TGH------LINPTNNNTMDSSFAGAYKYAVSNGIKTDNVY 347
                                                                                                                                SIKGVYVRNGANPLHEPVTGHHFFDGDGMVHAVKFEHGSASY--ACRFTQTNRFVQERQL 205
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                                                                                                                                                                                                                                                                                                                             LNPATGVMIPGSLGPSEQTPFSPEIEDGGIIPPEVAAANADKFKLSIPPSVPESIPEKDQ 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.7%; Score 116.5; DB 3; 19.9%; Pred. No. 0.0098; tive 74; Mismatches 175;
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RESULT 7
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                                                                                                        TELEFAX: 650-324-1678 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 650-324-1677
                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
MOLECULE TYPE:
                                                                                       SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 48
                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 12-SEP-1997
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                  TOPOLOGY:
                                STRANDEDNESS
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                                                                                                                                          TELEPHONE:
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                                                                      CENGTH:
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                                                                    1837 amino acids
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PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES INFECTIONS
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US-09-461-697-77
; Sequence 77, Applica;
; Patent No. 6277974
; GENERAL INFORMATION:
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Best Local Simi
Matches 113;
SEQ ID NO 77
LENGTH: 412
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                 APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart I
APPLICANT: Puranam, Kasturi
APPLICANT: Katz, Lawrence C.
                                                                                             CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
                                                                                                                                                        TITLE OF INVENTION: COMPOSITIONS AND METHODS TITLE OF INVENTION: AND TREATING CONDITIONS, TITLE OF INVENTION: CELL DEATH FILE REFERENCE: 10001-005-999
                                                                                                                                                                                                                                                                                                                                  APPLICANT: COGENT NEUROSCIENCE, APPLICANT: Lo, Donald C.
                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                               SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          985 LNPATGYMIPGSLGPSEQTPFSPEIEDGGIIPPEVAAANADKFKLSIPPSVPESIPEKDQ 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VTNTQYSNTTGNIINPETGKV--IPGSLPGSLNYPSFNTPQQTDE-----ITGKPVDT 1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TMMHDFAITENFVVVPDQQVVFKLPEMIRG-----GSPVVYDKNKVARFGILDKYAED 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGIV-SGKRGLPPIEDE-----NGNLFDPSTKLPIDGNNQL-----VNPETN 1223
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                                                                           SEQ ID NOS: 466
FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                            Barney,
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RESULT 9
US-08-611-107-31
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Best Local Sim
Matches 74;
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                    NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARCD:221
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/09340
FILING DATE: 30-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                  FILING DATE: 14-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US S
FILING DATE: 02-OCT-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FDCANESVLETLTDVAHEYCLKFTKLLRFAVDREARLGQTPFPDVMEQVFHEVGIGSVLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             United States of America
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                                                                                                                                                                                                 US SN 08/422,560
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; Sequence 106, Application
; Patent No. 6245331
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                    SOFTWARE: Pa
SEQ ID NO 106
LENGTH: 741
TYPE: PRT
                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 118; Conserv
                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/001,984C CURRENT FILING DATE: 1997-12-31
                                                                                                                                                                                                                                       APPLICANT: Belisle, John T
TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
                                                                                                                                PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1996-12-31
                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                     FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 2172 amino acid
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
ORGANISM: Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1876 FSGGQRDLFEGILQAGXMIVENLRTYKQPAFVYIPKAGELRGGAWVVVDSKI 1927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YSSQMQL---GGPKIMATNGVVHLTVSDDLEGVSAILKWL-----SYVPPYVG 1781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNMLGRKTKFAYLALAEPWPK--VSGFAKVDLTTGEVKKHLYGDNRYGGEPLFLPG----
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                                                                                       PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                  Laal, Suman
Zolla-Pazner, Susan
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19.9%; Pred. No. 0.65;
htive 80; Mismatches
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                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08097829 Patent No. 5498831 GENERAL INFORMATION:
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Best Local
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COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                              NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 200
                                                                                                                                                                                                                         APPLICANT: Burgess, Diane G.
APPLICANT: Dooner, Hugo K.
TITLE OF INVENTION: Pea ADP-Glucose Pyrophosphorylase
TITLE OF INVENTION: Genes and Their Uses
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                                                                                                             CITY: San Francisco
STATE: California
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Pred. No. 0.47;
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LENGTH: 516 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MASFTATAAVSGRWLGGNHTQPPLSSSQSSDLSYCSSLPMASRVTRKLNVSSA-----L 54
                                                                                                    DSSNIKWIDAPDCFCFHLWNAWEEPE----TDEVVVIGSCMTPPDSI 437
                                                                                                                                                                           VFKLPEMI ----
                                                                                                                                                                                                              GITKKPVPDFSFYDRSSPIYTQP-----RYLPPSKMLDADITDSVIGEGCVIKNCKIHHS
                                                                                                                                                                                                                                             -VVSKP---YLKYFRESPDGTKSPDVEIQLDQPTMMHDFAITENFV----VVPDQQV---
                                                                                                                                                                                                                                                                                LLRDKFPGANDFGSE------VIPGATELGLRVQAYLYDGYWEDIGTIEAFYNANL
                                                                                                                                                                                                                                                                                                                 L---KTVGRFDFDGQLESTMIAHPKVDPESGEL----FALSYD-----
                                                                                                                                                                                                                                                                                                                                                                                                                       DHLYRMDYER-----FIQAHRESDADITVASLPMDEARATA------FGLMK 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----RFVQERQLGRPVFPKAIGELHGHTGIARLMLFYARAAAGIVDPAHGTGVANAGLVY 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSRAYASNLGGYKNEGFVEVLAAQQSPENPNWFQGTADAVRQYLWLFEEHNVLEYLVLAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FT---VSGTRRSSGRNPFIVSPKAVSDSKNSQTCLDPDASRSVL----GIILGGGAGTRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTPPALHFPKQSSNSPAIVVKPKA-KESNTKQMNLFQRAAAAALDAAEGFLV---SHEKL 110
                                                                                                                                       VVGLRSCISEGAIIEDTLLMGADYYETDADRRFLAAKGGVPIGIGKNSHIKRAIIDKNAR
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GY: linear
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Pred. No.
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                                                                                                                                                                          -----RGGSPVVYDKNKVARFGILDKYAE 394
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Sequence 4, Application US/08577403 Patent No. 5773693

GENERAL INFORMATION:
APPLICANT: Burges
APPLICANT: Dooner

Burgess,

, Diane Hugo K.

Dooner,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 516 amino acid
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NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 22-DEC-
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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                             -VVSKP---YLKYFRESPDGTKSPDVEIQLDQPTMMHDFAITENEV----VVPDQQV----
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                                                                                                                                                                                                                                                                                                   F-----FDGDGMVHAVKFE-----HGSA----SYACRFTQTN------
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GITKKPVPDFSFYDRSSPIYTQP-----RYLPPSKMLDADITDSVIGEGCVIKNCKIHHS
                                                              LLRDKFPGANDFGSE------VIPGATELGLRVQAYLYDGYWEDIGTIEAFYNANL
                                                                                                 L---KTVGRFDFDGQLESTMIAHPKVDPESGEL----FALSYD--
                                                                                                                                  IDEEGRIVEFSEKPKGEQLKAMKVDTTILGLDDERAKEMPY---IASMGIYVVSKHVMLD
                                                                                                                                                                   FN--GRLLAMSE-----
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                                                                                                                                                                                                                             RFVQERQLGRPVFPKAIGELHGHTGIARLMLFYARAAAGIVDPAHGTGVANAGLVY 253
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20.9%;
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Pred. No.
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                                                                                                                                                               ----DD-----LPYQVQITPNG------
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US-09-335-409-3
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SEQ ID NO 3
LENGTH: 1410
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Best Local Similarity
Matches: 107; Conserv
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APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/335,409
CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
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APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
1015 RHGLRRDLDGKPVVDLTGQDPREAGLDVYARRRSVRTFLEAP 1056
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                                                                                                          LSYDVVSKPYLKYFRFSPDGTKSPDVEIQLDQPTMMHDFA--ITENFVVVPDQQVVFKLP 367
                                                                                                                                                                                                                                                                  GRPVFPKAIGELH-GHTGIARLMLFYAR----AAAGIVDPAHGTGVANAGLVYFNGRLL
                                                                                                                                                                                                                                                                                                       IWSIGYPVRN--
                                                                                                                                                                                                                                                                                                                                                                                                                   DAAEGFLVSHEKLHP--LPKTADPSVQIAGNFAPV----NEQPVRRNLPVV----GKLPDS 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPALHFPKQSSNS-----AL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSGRWLGGNHTQPPLSSSQS-SDLSY-----CSSLPMASRVTRK-----LNVSSALHT
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                                     EM-IR--
                                                                        VGNDAANKLLLAY--VVPEGTRRRAAEQDASLKTERIDARAHAAEADGLSDGERVQFKLA 1014
                                                                                                                                                                                       AMSEDDLPYQVQITPNGDLKTVGRFDFD---
                                                                                                                                                                                                                          PRPVW--VPGQLYIGGVGLA---LGYWRDEEKTRKSFLVHPETGERLYKTGDL---GRYL
                                                                                                                                                                                                                                                                                                                                          I--KGVYVRNGANPLHEPVTGHHFFDGDGMVHAVKFEHGSASYACRF-TQTNRFVQERQL 205
                                                                                                                                                                                                                                                                                                                                                                                PALMRMLVEHFEGRPDSLARSLRLSL-LSGDWIPVGLPGELQAIRPGVSVISLGGATEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPGDRVLALSSLSFDLSVYDVFGILAAGGTIVVPDASKLRDPAHWAELIEREKVTVWNSV 764
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                                   -GGSPVVYDKNKVARFGILDKYAEDSSNIKWIDAP
                                                                                                                                                 -PDGNIEFMGREDNQIKLRGYRVELGEIEETLKSHPNV--RDAVIVP
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23.2%; Pred. No. 2
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                                                                                                                                                                                                                                                                                                       VDLSWASIPYGRPLRNQTFHVLDEALE
                                                                                                                                                                                       ----GQLESTMIAHPKVDPESGELFA 309
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RESULT 14 US-09-568-102-3

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RESULT 15
US-09-567-969-3
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                                                                                                                              GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istv
                                                                                                                                                                                                                                                                    Sequence 3, Application US/09567969 Patent No. 6355457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 107;
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Best Local Similarity 23.2%;
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APPLICANT: GGETIACH, JOSETN
APPLICANT: GGETIACH, JOSETN
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/568,102
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ. ID NOS: 30
COUNTY OF THE PRIOR OF THE
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                                     APPLICANT:
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CANT: Cyr, Devon
CANT: Goerlach, Joern
OF INVENTION: GENES F
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Zirkle, Ross
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57; Mismatches 182; Indels 116;
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1410
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
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CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
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                                EM-IR---GGSPVVYDKNKVARFGILDKYAEDSSNIKWIDAP 405
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Pred. No. 2.
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